



#4

1

SEQUENCE LISTING

<110> GEORGE, LISLE W
ANGELOS, JOHN A
HESS, JOHN F

<120> MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES
AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA
BOVIS INFECTIONS

<130> 481.06

<140> 09/884,696

<141> 2001-06-19

<160> 41

<170> PatentIn Ver. 2.1

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<211> 2784

<212> DNA

<213> Moraxella bovis

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Ser	Thr	Lys	Ser	Gly	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Ile	Pro	Lys	Asp	
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tat	gat	ccg	caa	aaa	ggg	ggg	act	tta	aat	gat	ttt	att	aaa	gct	gct	144
Tyr	Asp	Pro	Gln	Lys	Gly	Gly	Thr	Leu	Asn	Asp	Phe	Ile	Lys	Ala	Ala	
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gat	gaa	tta	ggg	att	gct	cgt	tta	gca	gaa	gag	cct	aat	cac	act	gaa	192
Asp	Glu	Leu	Gly	Ile	Ala	Arg	Leu	Ala	Glu	Glu	Pro	Asn	His	Thr	Glu	
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aca	gca	aaa	aaa	tct	gtt	gac	aca	gta	aat	cag	ttt	ctc	tct	ctc	aca	240
Thr	Ala	Lys	Lys	Ser	Val	Asp	Thr	Val	Asn	Gln	Phe	Leu	Ser	Leu	Thr	
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Gln	Thr	Gly	Ile	Ala	Ile	Ser	Ala	Thr	Lys	Leu	Glu	Lys	Phe	Leu	Gln	
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Ile Asp Arg Lys Leu Gly Lys Ala Ser Asn Val Leu Ser Thr Leu Ser	
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Ser Phe Leu Gly Thr Ala Leu Ala Gly Ile Glu Leu Asp Ser Leu Ile	
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Lys Lys Gly Asp Ala Ala Pro Asp Ala Leu Ala Lys Ala Ser Ile Asp	
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ttg att aat gag ata att ggt aat cta tct cag agt act caa acg att	528
Leu Ile Asn Glu Ile Ile Gly Asn Leu Ser Gln Ser Thr Gln Thr Ile	
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Glu Ala Phe Ser Ser Gln Leu Ala Lys Leu Gly Ser Thr Ile Ser Gln	
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gct aaa ggc ttc tct aat ata gga aac aag ttg caa aac tta aat ttt	624
Ala Lys Gly Phe Ser Asn Ile Gly Asn Lys Leu Gln Asn Leu Asn Phe	
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Ser Lys Thr Asn Leu Gly Leu Glu Ile Ile Thr Gly Leu Leu Ser Gly	
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Lys Val Ala Ala Gly Phe Glu Leu Ser Asn Gln Val Ile Gly Asn Val	
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Thr Lys Ala Ile Ser Ser Tyr Val Leu Ala Gln Arg Val Ala Ala Gly	
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Leu Ser Thr Thr Gly Ala Val Ala Ala Leu Ile Thr Ser Ser Ile Met	
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Thr Asp Glu Ile Gly Leu Ile Val Asn Ala Lys Ala Gly Asn Asp Asp	
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Ile Phe Val Gly Gln Gly Lys Met Asn Ile Asp Gly Gly Asp Gly His	
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Asp Arg Val Phe Tyr Ser Lys Asp Gly Gly Phe Gly Asn Ile Thr Val	
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Val Ala Arg Gly Asp Ile Tyr His Glu Val Val Lys Arg Gln Glu Thr	
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Gly Ala Gly Asp Asp Arg Leu Phe Gly Gly Lys Gly Asn Asp Arg Leu	
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Ser Gly Asp Glu Gly Asp Asp Leu Leu Asp Gly Gly Ser Gly Asp Asp	
740 745 750	
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Val Leu Asn Gly Gly Ala Gly Asn Asp Val Tyr Ile Phe Arg Lys Gly	
755 760 765	
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Asp Gly Asn Asp Thr Leu Tyr Asp Gly Thr Gly Asn Asp Lys Leu Ala	
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Phe Ala Asp Ala Asn Ile Ser Asp Ile Met Ile Glu Arg Thr Lys Glu	
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Gly Ile Ile Val Lys Arg Asn Asp His Ser Gly Ser Ile Asn Ile Pro	
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aga tgg tac ata aca tca aat tta caa aat tat caa agt aat aaa aca	2496
Arg Trp Tyr Ile Thr Ser Asn Leu Gln Asn Tyr Gln Ser Asn Lys Thr	
820 825 830	
gat cat aaa att gag caa cta att ggt aaa gat ggt agt tat atc act	2544
Asp His Lys Ile Glu Gln Leu Ile Gly Lys Asp Gly Ser Tyr Ile Thr	
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Ser Asp Gln Ile Asp Lys Ile Leu Gln Asp Lys Lys Asp Gly Thr Val	
850 855 860	
att aca tct caa gaa ttg aaa aag ctt gct gat gag aat aag agc caa	2640
Ile Thr Ser Gln Glu Leu Lys Lys Leu Ala Asp Glu Asn Lys Ser Gln	
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Lys Leu Ser Ala Ser Asp Ile Ala Ser Ser Leu Asn Lys Leu Val Gly	
885 890 895	
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cag cca att aca caa cca act caa gga att ttg gct cca agt gtt tag	2784
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<213> Moraxella bovis

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Asp Glu Leu Gly Ile Ala Arg Leu Ala Glu Glu Pro Asn His Thr Glu	
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Gln Thr Gly Ile Ala Ile Ser Ala Thr Lys Leu Glu Lys Phe Leu Gln
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 Lys Lys Gly Asp Ala Ala Pro Asp Ala Leu Ala Lys Ala Ser Ile Asp
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 Leu Ile Asn Glu Ile Ile Gly Asn Leu Ser Gln Ser Thr Gln Thr Ile
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 Glu Ala Phe Ser Ser Gln Leu Ala Lys Leu Gly Ser Thr Ile Ser Gln
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 Ala Lys Gly Phe Ser Asn Ile Gly Asn Lys Leu Gln Asn Leu Asn Phe
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 Ser Lys Thr Asn Leu Gly Leu Glu Ile Ile Thr Gly Leu Leu Ser Gly
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 225 230 235 240
 Lys Val Ala Ala Gly Phe Glu Leu Ser Asn Gln Val Ile Gly Asn Val
 245 250 255
 Thr Lys Ala Ile Ser Ser Tyr Val Leu Ala Gln Arg Val Ala Ala Gly
 260 265 270
 Leu Ser Thr Thr Gly Ala Val Ala Ala Leu Ile Thr Ser Ser Ile Met
 275 280 285
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 290 295 300
 His Ala Asn Ala Leu Asp Glu Phe Ala Lys Gln Phe Arg Lys Phe Gly
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 Tyr Asp Gly Asp His Leu Leu Ala Glu Tyr Gln Arg Gly Val Gly Thr
 325 330 335
 Ile Glu Ala Ser Leu Thr Thr Ile Ser Thr Ala Leu Gly Ala Val Ser
 340 345 350
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 355 360 365
 Ala Leu Leu Val Ala Gly Val Thr Gly Leu Ile Ser Gly Ile Leu Glu
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Lys	Gly	Tyr	Asp	Ser	Arg	Tyr	Ala	Ala	Tyr	Leu	Ala	Asn	Asn	Leu	Lys	420	425	430	
Phe	Leu	Ser	Glu	Leu	Asn	Lys	Glu	Leu	Glu	Ala	Glu	Arg	Val	Ile	Ala	435	440	445	
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Thr	Lys	Leu	Gly	Glu	Arg	Ile	Lys	Ser	Gly	Lys	Ala	Tyr	Ala	Asp	Ala	465	470	475	480
Phe	Glu	Asp	Gly	Lys	Lys	Val	Glu	Ala	Gly	Ser	Asn	Ile	Thr	Leu	Asp	485	490	495	
Ala	Lys	Thr	Gly	Ile	Ile	Asp	Ile	Ser	Asn	Ser	Asn	Gly	Lys	Lys	Thr	500	505	510	
Gln	Ala	Leu	His	Phe	Thr	Ser	Pro	Leu	Leu	Thr	Ala	Gly	Thr	Glu	Ser	515	520	525	
Arg	Glu	Arg	Leu	Thr	Asn	Gly	Lys	Tyr	Ser	Tyr	Ile	Asn	Lys	Leu	Lys	530	535	540	
Phe	Gly	Arg	Val	Lys	Asn	Trp	Gln	Val	Thr	Asp	Gly	Glu	Ala	Ser	Ser	545	550	555	560
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Thr	Asp	Glu	Ile	Gly	Leu	Ile	Val	Asn	Ala	Lys	Ala	Gly	Asn	Asp	Asp	580	585	590	
Ile	Phe	Val	Gly	Gln	Gly	Lys	Met	Asn	Ile	Asp	Gly	Gly	Asp	Gly	His	595	600	605	
Asp	Arg	Val	Phe	Tyr	Ser	Lys	Asp	Gly	Gly	Phe	Gly	Asn	Ile	Thr	Val	610	615	620	
Asp	Gly	Thr	Ser	Ala	Thr	Glu	Ala	Gly	Ser	Tyr	Thr	Val	Asn	Arg	Lys	625	630	635	640
Val	Ala	Arg	Gly	Asp	Ile	Tyr	His	Glu	Val	Val	Lys	Arg	Gln	Glu	Thr	645	650	655	
Lys	Val	Gly	Lys	Arg	Thr	Glu	Thr	Ile	Gln	Tyr	Arg	Asp	Tyr	Glu	Leu	660	665	670	
Arg	Lys	Val	Gly	Tyr	Gly	Tyr	Gln	Ser	Thr	Asp	Asn	Leu	Lys	Ser	Val	675	680	685	

Glu Glu Val Ile Gly Ser Gln Phe Asn Asp Val Phe Lys Gly Ser Lys
 690 695 700
 Phe Asn Asp Ile Phe His Ser Gly Glu Gly Asp Asp Leu Leu Asp Gly
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 725 730 735
 Ser Gly Asp Glu Gly Asp Asp Leu Leu Asp Gly Gly Ser Gly Asp Asp
 740 745 750
 Val Leu Asn Gly Gly Ala Gly Asn Asp Val Tyr Ile Phe Arg Lys Gly
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 Asp Gly Asn Asp Thr Leu Tyr Asp Gly Thr Gly Asn Asp Lys Leu Ala
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 Phe Ala Asp Ala Asn Ile Ser Asp Ile Met Ile Glu Arg Thr Lys Glu
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 Gly Ile Ile Val Lys Arg Asn Asp His Ser Gly Ser Ile Asn Ile Pro
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 Ser Asp Gln Ile Asp Lys Ile Leu Gln Asp Lys Lys Asp Gly Thr Val
 850 855 860
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<212> PRT

<213> Pasteurella haemolytica

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 Pro Gln Asn Tyr Gln Tyr Asp Thr Glu Gln Gly Asn Gly Leu Gln Asp
 50 55 60
 Leu Val Lys Ala Ala Glu Leu Gly Ile Glu Val Gln Arg Glu Glu
 65 70 75 80
 Arg Asn Asn Ile Ala Thr Ala Gln Thr Ser Leu Gly Thr Ile Gln Thr
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 Ala Ile Gly Leu Thr Glu Arg Gly Ile Val Leu Ser Ala Pro Gln Ile
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 Ala Leu Gln Asn Asn Ser Asn Gln His Ala Leu Ala Lys Ala Gly Leu
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 245 250 255
 Ala Lys Lys Val Gly Ala Gly Phe Glu Leu Ala Asn Gln Val Val Gly
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 Asn Ile Thr Lys Ala Val Ser Ser Tyr Ile Leu Ala Gln Arg Val Ala
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 Ala Gly Leu Ser Ser Thr Gly Pro Val Ala Ala Leu Ile Ala Ser Thr
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 Val Ser Leu Ala Ile Ser Pro Leu Ala Phe Ala Gly Ile Ala Asp Lys
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 Phe Asn His Ala Lys Ser Leu Glu Ser Tyr Ala Glu Arg Phe Lys Lys
 325 330 335

Leu Gly Tyr Asp Gly Asp Asn Leu Leu Ala Glu Tyr Gln Arg Gly Thr
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 Gly Thr Ile Asp Ala Ser Val Thr Ala Ile Asn Thr Ala Leu Ala Ala
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 Ile Ala Gly Gly Val Ser Ala Ala Ala Gly Ser Val Ile Ala Ser
 370 375 380
 Pro Ile Ala Leu Leu Val Ser Gly Ile Thr Gly Val Ile Ser Thr Ile
 385 390 395 400
 Leu Gln Tyr Ser Lys Gln Ala Met Phe Glu His Val Ala Asn Lys Ile
 405 410 415
 His Asn Lys Ile Val Glu Trp Glu Lys Asn Asn His Gly Lys Asn Tyr
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 Gly Ile Ser Arg Leu Gly Glu Lys Val Leu Ser Gly Lys Ala Tyr Val
 485 490 495
 Asp Ala Phe Glu Glu Gly Lys His Ile Lys Ala Asp Lys Leu Val Gln
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 Lys Thr Gln His Ile Leu Phe Arg Thr Pro Leu Leu Thr Pro Gly Thr
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 Glu His Arg Glu Arg Val Gln Thr Gly Lys Tyr Glu Tyr Ile Thr Lys
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 580 585 590
 Leu Asp Asn Ala Gly Asn Val Thr Lys Thr Lys Glu Thr Lys Ile Ile
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 Ala Lys Leu Gly Glu Gly Asp Asp Asn Val Phe Val Gly Ser Gly Thr
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 Thr Glu Ile Asp Gly Gly Glu Gly Tyr Asp Arg Val His Tyr Ser Arg
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Gly	Lys	Gly	Asp	Asp	Ile	Leu	Asp	Gly	Gly	Asn	Gly	Asp	Asp	Phe	Ile	
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Asp	Gly	Gly	Lys	Gly	Asn	Asp	Leu	Leu	His	Gly	Gly	Lys	Gly	Asp	Asp	
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785					790					795					800	
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Glu	Lys	Val	Thr	Ile	Gln	Asn	Trp	Phe	Arg	Glu	Ala	Asp	Phe	Ala	Lys	
		835					840					845				
Glu	Val	Pro	Asn	Tyr	Lys	Ala	Thr	Lys	Asp	Glu	Lys	Ile	Glu	Glu	Ile	
	850					855					860					
Ile	Gly	Gln	Asn	Gly	Glu	Arg	Ile	Thr	Ser	Lys	Gln	Val	Asp	Asp	Leu	
865					870					875					880	
Ile	Ala	Lys	Gly	Asn	Gly	Lys	Ile	Thr	Gln	Asp	Glu	Leu	Ser	Lys	Val	
				885					890					895		
Val	Asp	Asn	Tyr	Glu	Leu	Leu	Lys	His	Ser	Lys	Asn	Val	Thr	Asn	Ser	
			900					905						910		
Leu	Asp	Lys	Leu	Ile	Ser	Ser	Val	Ser	Ala	Phe	Thr	Ser	Ser	Asn	Asp	
		915					920					925				
Ser	Arg	Asn	Val	Leu	Val	Ala	Pro	Thr	Ser	Met	Leu	Asp	Gln	Ser	Leu	
	930					935					940					

Ser Ser Leu Gln Phe Ala Arg Ala Ala
945 950

<210> 4

<211> 956

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 4

Met Ser Lys Ile Thr Leu Ser Ser Leu Lys Ser Ser Leu Gln Gln Gly
1 5 10 15

Leu Lys Asn Gly Lys Asn Lys Leu Asn Gln Ala Gly Thr Thr Leu Lys
20 25 30

Asn Gly Leu Thr Gln Thr Gly His Ser Leu Gln Asn Gly Ala Lys Lys
35 40 45

Leu Ile Leu Tyr Ile Pro Gln Gly Tyr Asp Ser Gly Gln Gly Asn Gly
50 55 60

Val Gln Asp Leu Val Lys Ala Ala Asn Asp Leu Gly Ile Glu Val Trp
65 70 75 80

Arg Glu Glu Arg Ser Asn Leu Asp Ile Ala Lys Thr Ser Phe Asp Thr
85 90 95

Thr Gln Lys Ile Leu Gly Phe Thr Asp Arg Gly Ile Val Leu Phe Ala
100 105 110

Pro Gln Leu Asp Asn Leu Leu Lys Lys Asn Pro Lys Ile Gly Asn Thr
115 120 125

Leu Gly Ser Ala Ser Ser Ile Ser Gln Asn Ile Gly Lys Ala Asn Thr
130 135 140

Val Leu Gly Gly Ile Gln Ser Ile Leu Gly Ser Val Leu Ser Gly Val
145 150 155 160

Asn Leu Asn Glu Leu Leu Gln Asn Lys Asp Pro Asn Gln Leu Glu Leu
165 170 175

Ala Lys Ala Gly Leu Glu Leu Thr Asn Glu Leu Val Gly Asn Ile Ala
180 185 190

Ser Ser Val Gln Thr Val Asp Ala Phe Ala Glu Gln Ile Ser Lys Leu
195 200 205

Gly Ser His Leu Gln Asn Val Lys Gly Leu Gly Gly Leu Ser Asn Lys
210 215 220

Leu Gln Asn Leu Pro Asp Leu Gly Lys Ala Ser Leu Gly Leu Asp Ile
225 230 235 240

Ile Ser Gly Leu Leu Ser Gly Ala Ser Ala Gly Leu Ile Leu Ala Asp
245 250 255

Lys	Glu	Ala	Ser	Thr	Glu	Lys	Lys	Ala	Ala	Ala	Gly	Val	Glu	Phe	Ala	
			260					265					270			
Asn	Gln	Ile	Ile	Gly	Asn	Val	Thr	Lys	Ala	Val	Ser	Ser	Tyr	Ile	Leu	
		275					280					285				
Ala	Gln	Arg	Val	Ala	Ser	Gly	Leu	Ser	Ser	Thr	Gly	Pro	Val	Ala	Ala	
	290					295					300					
Leu	Ile	Ala	Ser	Thr	Val	Ala	Leu	Ala	Val	Ser	Pro	Leu	Ser	Phe	Leu	
305					310					315					320	
Asn	Val	Ala	Asp	Lys	Phe	Lys	Gln	Ala	Asp	Leu	Ile	Lys	Ser	Tyr	Ser	
			325						330					335		
Glu	Arg	Phe	Gln	Lys	Leu	Gly	Tyr	Asp	Gly	Asp	Arg	Leu	Leu	Ala	Asp	
			340					345					350			
Phe	His	Arg	Glu	Thr	Gly	Thr	Ile	Asp	Ala	Ser	Val	Thr	Thr	Ile	Asn	
		355					360					365				
Thr	Ala	Leu	Ala	Ala	Ile	Ser	Gly	Gly	Val	Gly	Ala	Ala	Ser	Ala	Gly	
	370					375					380					
Ser	Leu	Val	Gly	Ala	Pro	Val	Ala	Leu	Leu	Val	Ala	Gly	Val	Thr	Gly	
385					390					395					400	
Leu	Ile	Thr	Thr	Ile	Leu	Glu	Tyr	Ser	Lys	Gln	Ala	Met	Phe	Glu	His	
				405					410					415		
Val	Ala	Asn	Lys	Val	His	Asp	Arg	Ile	Val	Glu	Trp	Glu	Lys	Lys	His	
			420					425					430			
Asn	Lys	Asn	Tyr	Phe	Glu	Gln	Gly	Tyr	Asp	Ser	Arg	His	Leu	Ala	Asp	
		435					440					445				
Leu	Gln	Asp	Asn	Met	Lys	Phe	Leu	Ile	Asn	Leu	Asn	Lys	Glu	Leu	Gln	
	450					455					460					
Ala	Glu	Arg	Val	Val	Ala	Ile	Thr	Gln	Gln	Arg	Trp	Asp	Asn	Gln	Ile	
465					470					475					480	
Gly	Asp	Leu	Ala	Ala	Ile	Ser	Arg	Arg	Thr	Asp	Lys	Ile	Ser	Ser	Gly	
				485					490					495		
Lys	Ala	Tyr	Val	Asp	Ala	Phe	Glu	Glu	Gly	Gln	His	Gln	Ser	Tyr	Asp	
			500					505					510			
Ser	Ser	Val	Gln	Leu	Asp	Asn	Lys	Asn	Gly	Ile	Ile	Asn	Ile	Ser	Asn	
		515					520					525				
Thr	Asn	Arg	Lys	Thr	Gln	Ser	Val	Leu	Phe	Arg	Thr	Pro	Leu	Leu	Thr	
	530					535					540					
Pro	Gly	Glu	Glu	Asn	Arg	Glu	Arg	Ile	Gln	Glu	Gly	Lys	Asn	Ser	Tyr	
545					550					555					560	

Ile Thr Lys Leu His Ile Gln Arg Val Asp Ser Trp Thr Val Thr Asp
 565 570 575
 Gly Asp Ala Ser Ser Ser Val Asp Phe Thr Asn Val Val Gln Arg Ile
 580 585 590
 Ala Val Lys Phe Asp Asp Ala Gly Asn Ile Ile Glu Ser Lys Asp Thr
 595 600 605
 Lys Ile Ile Ala Asn Leu Gly Ala Gly Asn Asp Asn Val Phe Val Gly
 610 615 620
 Ser Ser Thr Thr Val Ile Asp Gly Gly Asp Gly His Asp Arg Val His
 625 630 635 640
 Tyr Ser Arg Gly Glu Tyr Gly Ala Leu Val Ile Asp Ala Thr Ala Glu
 645 650 655
 Thr Glu Lys Gly Ser Tyr Ser Val Lys Arg Tyr Val Gly Asp Ser Lys
 660 665 670
 Ala Leu His Glu Thr Ile Ala Thr His Gln Thr Asn Val Gly Asn Arg
 675 680 685
 Glu Glu Lys Ile Glu Tyr Arg Arg Glu Asp Asp Arg Phe His Thr Gly
 690 695 700
 Tyr Thr Val Thr Asp Ser Leu Lys Ser Val Glu Glu Ile Ile Gly Ser
 705 710 715 720
 Gln Phe Asn Asp Ile Phe Lys Gly Ser Gln Phe Asp Asp Val Phe His
 725 730 735
 Gly Gly Asn Gly Val Asp Thr Ile Asp Gly Asn Asp Gly Asp Asp His
 740 745 750
 Leu Phe Gly Gly Ala Gly Asp Asp Val Ile Asp Gly Gly Asn Gly Asn
 755 760 765
 Asn Phe Leu Val Gly Gly Thr Gly Asn Asp Ile Ile Ser Gly Gly Lys
 770 775 780
 Asp Asn Asp Ile Tyr Val His Lys Thr Gly Asp Gly Asn Asp Ser Ile
 785 790 795 800
 Thr Asp Ser Gly Gly Gln Asp Lys Leu Ala Phe Ser Asp Val Asn Leu
 805 810 815
 Lys Asp Leu Thr Phe Lys Lys Val Asp Ser Ser Leu Glu Ile Ile Asn
 820 825 830
 Gln Lys Gly Glu Lys Val Arg Ile Gly Asn Trp Phe Leu Glu Asp Asp
 835 840 845
 Leu Ala Ser Thr Val Ala Asn Tyr Lys Ala Thr Asn Asp Arg Lys Ile
 850 855 860

Glu Glu Ile Ile Gly Lys Gly Gly Glu Arg Ile Thr Ser Glu Gln Val
865 870 875 880

Asp Lys Leu Ile Lys Glu Gly Asn Asn Gln Ile Ser Ala Glu Ala Leu
885 890 895

Ser Lys Val Val Asn Asp Tyr Asn Thr Ser Lys Asp Arg Gln Asn Val
900 905 910

Ser Asn Ser Leu Ala Lys Leu Ile Ser Ser Val Gly Ser Phe Thr Ser
915 920 925

Ser Ser Asp Phe Arg Asn Asn Leu Gly Thr Tyr Val Pro Ser Ser Ile
930 935 940

Asp Val Ser Asn Asn Ile Gln Leu Ala Arg Ala Ala
945 950 955

<210> 5

<211> 1023

<212> PRT

<213> Escherichia coli

<400> 5

Met Pro Thr Ile Thr Ala Ala Gln Ile Lys Ser Thr Leu Gln Ser Ala
1 5 10 15

Lys Gln Ser Ala Ala Asn Lys Leu His Ser Ala Gly Gln Ser Thr Lys
20 25 30

Asp Ala Leu Lys Lys Ala Ala Glu Gln Thr Arg Asn Ala Gly Asn Arg
35 40 45

Leu Ile Leu Leu Ile Pro Lys Asp Tyr Lys Gly Gln Gly Ser Ser Leu
50 55 60

Asn Asp Leu Val Arg Thr Ala Asp Glu Leu Gly Ile Glu Val Gln Tyr
65 70 75 80

Asp Glu Lys Asn Gly Thr Ala Ile Thr Lys Gln Val Phe Gly Thr Ala
85 90 95

Glu Lys Leu Ile Gly Leu Thr Glu Arg Gly Val Thr Ile Phe Ala Pro
100 105 110

Gln Leu Asp Lys Leu Leu Gln Lys Tyr Gln Lys Ala Gly Asn Lys Leu
115 120 125

Gly Gly Ser Ala Glu Asn Ile Gly Asp Asn Leu Gly Lys Ala Gly Ser
130 135 140

Val Leu Ser Thr Phe Gln Asn Phe Leu Gly Thr Ala Leu Ser Ser Met
145 150 155 160

Lys Ile Asp Glu Leu Ile Lys Lys Gln Lys Ser Gly Gly Asn Val Ser
165 170 175

Ser Ser Glu Leu Ala Lys Ala Ser Ile Glu Leu Ile Asn Gln Leu Val
 180 185 190
 Asp Thr Ala Ala Ser Leu Asn Asn Val Asn Ser Phe Ser Gln Gln Leu
 195 200 205
 Asn Lys Leu Gly Ser Val Leu Ser Asn Thr Lys His Leu Asn Gly Val
 210 215 220
 Gly Asn Lys Leu Gln Asn Leu Pro Asn Leu Asp Asn Ile Gly Ala Gly
 225 230 235 240
 Leu Asp Thr Val Ser Gly Ile Leu Ser Ala Ile Ser Ala Ser Phe Ile
 245 250 255
 Leu Ser Asn Ala Asp Ala Asp Thr Gly Thr Lys Ala Ala Ala Gly Val
 260 265 270
 Glu Leu Thr Thr Lys Val Leu Gly Asn Val Gly Lys Gly Ile Ser Gln
 275 280 285
 Tyr Ile Ile Ala Gln Arg Ala Ala Gln Gly Leu Ser Thr Ser Ala Ala
 290 295 300
 Ala Ala Gly Leu Ile Ala Ser Val Val Thr Leu Ala Ile Ser Pro Leu
 305 310 315 320
 Ser Phe Leu Ser Ile Ala Asp Lys Phe Lys Arg Ala Asn Lys Ile Glu
 325 330 335
 Glu Tyr Ser Gln Arg Phe Lys Lys Leu Gly Tyr Asp Gly Asp Ser Leu
 340 345 350
 Leu Ala Ala Phe His Lys Glu Thr Gly Ala Ile Asp Ala Ser Leu Thr
 355 360 365
 Arg Ile Ser Thr Val Leu Ala Ser Val Ser Ser Gly Ile Ser Ala Ala
 370 375 380
 Ala Thr Thr Ser Leu Val Gly Ala Pro Val Ser Ala Leu Val Gly Ala
 385 390 395 400
 Val Thr Gly Ile Ile Ser Gly Ile Leu Glu Ala Ser Lys Gln Ala Met
 405 410 415
 Phe Glu His Val Ala Ser Lys Met Ala Asp Val Ile Ala Glu Trp Glu
 420 425 430
 Lys Lys His Gly Lys Asn Tyr Phe Glu Asn Gly Tyr Asp Ala Arg His
 435 440 445
 Ala Ala Phe Leu Glu Asp Asn Phe Lys Ile Leu Ser Gln Tyr Asn Lys
 450 455 460
 Glu Tyr Ser Val Glu Arg Ser Val Leu Ile Thr Gln Gln His Trp Asp
 465 470 475 480

Thr Leu Ile Gly Glu Leu Ala Gly Val Thr Arg Asn Gly Asp Lys Thr
 485 490 495
 Leu Ser Gly Lys Ser Tyr Ile Asp Tyr Tyr Glu Glu Gly Lys Arg Leu
 500 505 510
 Glu Lys Lys Pro Asp Glu Phe Gln Lys Gln Val Phe Asp Pro Leu Lys
 515 520 525
 Gly Asn Ile Asp Leu Ser Asp Ser Lys Ser Ser Thr Leu Leu Lys Phe
 530 535 540
 Val Thr Pro Leu Leu Thr Pro Gly Glu Glu Ile Arg Glu Arg Arg Gln
 545 550 555 560
 Ser Gly Lys Tyr Glu Tyr Ile Thr Glu Leu Leu Val Lys Gly Val Asp
 565 570 575
 Lys Trp Thr Val Lys Gly Val Gln Asp Lys Gly Ser Val Tyr Asp Tyr
 580 585 590
 Ser Asn Leu Ile Gln His Ala Ser Val Gly Asn Asn Gln Tyr Arg Glu
 595 600 605
 Ile Arg Ile Glu Ser His Leu Gly Asp Gly Asp Asp Lys Val Phe Leu
 610 615 620
 Ser Ala Gly Ser Ala Asn Ile Tyr Ala Gly Lys Gly His Asp Val Val
 625 630 635 640
 Tyr Tyr Asp Lys Thr Asp Thr Gly Tyr Leu Thr Ile Asp Gly Thr Lys
 645 650 655
 Ala Thr Glu Ala Gly Asn Tyr Thr Val Thr Arg Val Leu Gly Gly Asp
 660 665 670
 Val Lys Val Leu Gln Glu Val Val Lys Glu Gln Glu Val Ser Val Gly
 675 680 685
 Lys Arg Thr Glu Lys Thr Gln Tyr Arg Ser Tyr Glu Phe Thr His Ile
 690 695 700
 Asn Gly Lys Asn Leu Thr Glu Thr Asp Asn Leu Tyr Ser Val Glu Glu
 705 710 715 720
 Leu Ile Gly Thr Thr Arg Ala Asp Lys Phe Phe Gly Ser Lys Phe Ala
 725 730 735
 Asp Ile Phe His Gly Ala Asp Gly Asp Asp His Ile Glu Gly Asn Asp
 740 745 750
 Gly Asn Asp Arg Leu Tyr Gly Asp Lys Gly Asn Asp Thr Leu Ser Gly
 755 760 765
 Gly Asn Gly Asp Asp Gln Leu Tyr Gly Gly Asp Gly Asn Asp Lys Leu
 770 775 780

Ile Gly Gly Ala Gly Asn Asn Tyr Leu Asn Gly Gly Asp Gly Asp Asp
 785 790 795 800
 Glu Leu Gln Val Gln Gly Asn Ser Leu Ala Lys Asn Val Leu Ser Gly
 805 810 815
 Gly Lys Gly Asn Asp Lys Leu Tyr Gly Ser Glu Gly Ala Asp Leu Leu
 820 825 830
 Asp Gly Gly Glu Gly Asn Asp Leu Leu Lys Gly Gly Tyr Gly Asn Asp
 835 840 845
 Ile Tyr Arg Tyr Leu Ser Gly Tyr Gly His His Ile Ile Asp Asp Asp
 850 855 860
 Gly Gly Lys Asp Asp Lys Leu Ser Leu Ala Asp Ile Asp Phe Arg Asp
 865 870 875 880
 Val Ala Phe Arg Arg Glu Gly Asn Asp Leu Ile Met Tyr Lys Ala Glu
 885 890 895
 Gly Asn Val Leu Ser Ile Gly His Lys Asn Gly Ile Thr Phe Lys Asn
 900 905 910
 Trp Phe Glu Lys Glu Ser Gly Asp Ile Ser Asn His Gln Ile Glu Gln
 915 920 925
 Ile Phe Asp Lys Asp Gly Arg Val Ile Thr Pro Asp Ser Leu Lys Lys
 930 935 940
 Ala Leu Glu Tyr Gln Gln Ser Asn Asn Lys Ala Ser Tyr Val Tyr Gly
 945 950 955 960
 Asn Asp Ala Leu Ala Tyr Gly Ser Gln Gly Asn Leu Asn Pro Leu Ile
 965 970 975
 Asn Glu Ile Ser Lys Ile Ile Ser Ala Ala Gly Asn Phe Asp Val Lys
 980 985 990
 Glu Glu Arg Ala Ala Ala Ser Leu Leu Gln Leu Ser Gly Asn Ala Ser
 995 1000 1005
 Asp Phe Ser Tyr Gly Arg Asn Ser Ile Thr Leu Thr Ala Ser Ala
 1010 1015 1020

<210> 6
 <211> 12
 <212> PRT
 <213> Moraxella bovis

<400> 6
 Phe Leu Ser Glu Leu Asn Lys Glu Leu Glu Ala Glu
 1 5 10

<210> 7
 <211> 12

<212> PRT

<213> *Pasteurella haemolytica*

<400> 7

Phe Leu Leu Asn Leu Asn Lys Glu Leu Gln Ala Glu
1 5 10

<210> 8

<211> 12

<212> PRT

<213> *Escherichia coli*

<400> 8

Ile Leu Ser Gln Tyr Asn Lys Glu Tyr Ser Val Glu
1 5 10

<210> 9

<211> 12

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 9

Phe Leu Ile Asn Leu Asn Lys Glu Leu Gln Ala Glu
1 5 10

<210> 10

<211> 12

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 10

Leu Leu Ser Gln Tyr Asn Lys Glu Tyr Ser Val Glu
1 5 10

<210> 11

<211> 12

<212> PRT

<213> *Actinobacillus suis*

<400> 11

Phe Leu Ile Asn Leu Asn Lys Glu Leu Gln Ala Glu
1 5 10

<210> 12

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>
 <221> MOD_RES
 <222> (3)
 <223> L, Y, A or V

<220>
 <221> MOD_RES
 <222> (7)..(8)
 <223> L, Y, A or V

<400> 12
 Phe Leu Xaa Asn Lys Glu Xaa Xaa Glu
 1 5

<210> 13
 <211> 14
 <212> PRT
 <213> Moraxella bovis

<400> 13
 Phe Asn Asp Ile Phe His Ser Gly Glu Gly Asp Asp Leu Leu
 1 5 10

<210> 14
 <211> 14
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 14
 Phe Arg Asp Ile Phe His Gly Ala Asp Gly Asp Asp Leu Leu
 1 5 10

<210> 15
 <211> 14
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 15
 Phe Asn Asp Val Phe His Gly His Asp Gly Asp Asp Leu Ile
 1 5 10

<210> 16
 <211> 14
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 16
 Phe Arg Asp Ile Phe His Gly Ala Asp Gly Asp Asp Leu Leu
 1 5 10

<210> 17
 <211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>

<221> MOD_RES

<222> (11)

<223> L or I

<400> 17

Phe Asp Phe His Gly Ala Asp Gly Asp Asp Xaa
1 5 10

<210> 18

<211> 737

<212> PRT

<213> Moraxella bovis

<400> 18

Met Gly Gly Asp Thr Ser Leu Ile Arg Leu Asn Leu Gln Thr Leu Asn
1 5 10 15Ser Asn Leu Val Met Ile Asp Tyr Ala Gln Gln Pro Ala Leu Ser Ala
20 25 30Leu Val Ile Leu Ala Lys Tyr Tyr Gly Ile Ser Ala Ser Pro Ala Asp
35 40 45Ile Met His Gln Phe Ser Asp Asn Thr Lys Gly Asp Leu Asn Glu Ile
50 55 60Glu Trp Met Leu Ala Ala Lys Lys Leu Glu Leu Lys Val Lys Ile Ile
65 70 75 80Lys Gln Pro Leu Thr Arg Leu Ser Met Ile Thr Leu Pro Ala Leu Val
85 90 95Trp Cys Asp Asn Lys Pro Asp Leu Asp Gln Asn Leu Asn Ser His Phe
100 105 110Ile Leu Thr Lys Ile Asp Gly Val Gly Ser Ala Ala Lys Tyr Leu Ile
115 120 125Tyr Asp Leu Ile Glu Asn Arg Pro Ile Ile Leu Asp Ala Ser Glu Phe
130 135 140Ser Glu Arg Tyr Ser Gly Lys Leu Met Leu Val Thr Ser Arg Ala Ser
145 150 155 160Ile Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala
165 170 175Val Ile Lys Tyr Arg Tyr Ile Phe Phe Glu Val Ile Val Ile Ser Val
180 185 190

Val Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln Val Val
 195 200 205
 Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asp Val Val
 210 215 220
 Ala Ile Ala Leu Leu Val Val Ser Leu Phe Glu Val Ile Leu Ser Gly
 225 230 235 240
 Leu Arg Thr Tyr Ile Phe Ala His Thr Thr Ser Arg Ile Asp Val Glu
 245 250 255
 Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ala Leu Pro Leu Ala Tyr
 260 265 270
 Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Ile Arg Glu Leu
 275 280 285
 Glu His Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser Val Leu
 290 295 300
 Asp Leu Val Phe Ser Phe Ile Phe Leu Phe Val Met Trp Tyr Tyr Ser
 305 310 315 320
 Pro Thr Leu Thr Leu Val Val Leu Ala Ser Leu Pro Ile Tyr Ala Phe
 325 330 335
 Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr Arg Leu Asn Asp Gln
 340 345 350
 Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser Ile Thr
 355 360 365
 Ala Val Gly Thr Val Lys Ala Met Ala Val Glu Pro Gln Met Thr Arg
 370 375 380
 Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Val Ser Ser Phe Arg Val
 385 390 395 400
 Ala Lys Leu Ala Met Val Gly Gln Gln Gly Val Gln Leu Ile Gln Lys
 405 410 415
 Met Val Ile Val Ala Thr Leu Trp Ile Gly Ala Lys Leu Val Ile Glu
 420 425 430
 Gly Lys Leu Ser Val Gly Gln Leu Ile Ala Phe Asn Met Leu Ala Gly
 435 440 445
 Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln Asp Phe
 450 455 460
 Gln Gln Val Gly Ile Ser Val Ala Arg Leu Gly Asp Ile Leu Asn Thr
 465 470 475 480
 Pro Thr Glu His Ser Thr Ser Arg Leu Thr Leu Pro Asp Ile Lys Gly
 485 490 495

Asp Ile Thr Phe Glu Asn Val Asp Phe Arg Tyr Lys Ile Asp Gly His
 500 505 510
 Leu Ile Leu Gln Asn Leu Asn Leu Gln Ile Asn Ala Gly Glu Ile Leu
 515 520 525
 Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr Lys Leu
 530 535 540
 Val Gln Arg Leu Tyr Val Pro Glu Asn Gly Arg Ile Leu Val Asp Gly
 545 550 555 560
 Asn Asp Leu Ala Leu Ala Asp Pro Ala Trp Leu Arg Arg Gln Val Gly
 565 570 575
 Val Val Leu Gln Glu Asn Val Leu Leu Asn Arg Ser Ile Arg Asp Asn
 580 585 590
 Ile Ala Leu Thr Asp Thr Gly Met Ser Leu Glu Phe Ile Ile Gln Ala
 595 600 605
 Ala Lys Met Ser Gly Ala His Asp Phe Ile Met Glu Leu Pro Glu Gly
 610 615 620
 Tyr Asp Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly Gly Gln
 625 630 635 640
 Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Ile Thr Asn Pro Arg Ile
 645 650 655
 Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser Glu Arg
 660 665 670
 Ala Ile Met Gln Asn Met Gln Ala Ile Cys Gln Gly Arg Thr Val Leu
 675 680 685
 Ile Ile Ala His Arg Leu Ser Thr Val Lys Met Ala His Arg Ile Ile
 690 695 700
 Ala Met Asp Lys Gly Lys Ile Val Glu Gln Gly Thr His Gln Glu Leu
 705 710 715 720
 Leu Gln Lys Glu Asp Gly Tyr Tyr Arg Tyr Leu Tyr Asp Leu Gln Asn
 725 730 735

Gly

<210> 19

<211> 708

<212> PRT

<213> *Pasteurella haemolytica*

<400> 19

Met Glu Ala Asn His Gln Arg Asn Asp Leu Gly Leu Val Ala Leu Thr
 1 5 10 15

Met	Leu	Ala	Gln	Tyr	His	Asn	Ile	Ser	Leu	Asn	Pro	Glu	Glu	Ile	Lys	20	25	30
His	Lys	Phe	Asp	Leu	Asp	Gly	Lys	Gly	Leu	Ser	Leu	Thr	Ala	Trp	Leu	35	40	45
Leu	Ala	Ala	Lys	Ser	Leu	Ala	Leu	Lys	Ala	Lys	His	Ile	Lys	Lys	Glu	50	55	60
Ile	Ser	Arg	Leu	His	Leu	Val	Asn	Leu	Pro	Ala	Leu	Val	Trp	Gln	Asp	65	70	75
Asn	Gly	Lys	His	Phe	Leu	Leu	Val	Lys	Val	Asp	Thr	Asp	Asn	Asn	Arg	85	90	95
Tyr	Leu	Thr	Tyr	Asn	Leu	Glu	Gln	Asp	Ala	Pro	Gln	Ile	Leu	Ser	Thr	100	105	110
Asp	Glu	Phe	Glu	Ala	Cys	Tyr	Gln	Gly	Gln	Leu	Ile	Leu	Val	Thr	Ser	115	120	125
Arg	Ala	Ser	Val	Val	Gly	Gln	Leu	Ala	Lys	Phe	Asp	Phe	Thr	Trp	Phe	130	135	140
Ile	Pro	Ala	Val	Ile	Lys	Tyr	Arg	Lys	Ile	Phe	Leu	Glu	Thr	Leu	Ile	145	150	155
Val	Ser	Ile	Phe	Leu	Gln	Ile	Phe	Ala	Leu	Ile	Thr	Pro	Leu	Phe	Phe	165	170	175
Gln	Val	Val	Met	Asp	Lys	Val	Leu	Val	His	Arg	Gly	Phe	Ser	Thr	Leu	180	185	190
Asn	Ile	Ile	Thr	Val	Ala	Leu	Ala	Ile	Val	Ile	Ile	Phe	Glu	Ile	Val	195	200	205
Leu	Ser	Gly	Leu	Arg	Thr	Tyr	Val	Phe	Ser	His	Ser	Thr	Ser	Arg	Ile	210	215	220
Asp	Val	Glu	Leu	Gly	Ala	Lys	Leu	Phe	Arg	His	Leu	Leu	Ser	Leu	Pro	225	230	235
Ile	Ser	Tyr	Phe	Glu	Asn	Arg	Arg	Val	Gly	Asp	Thr	Val	Ala	Arg	Val	245	250	255
Arg	Glu	Leu	Asp	Gln	Ile	Arg	Asn	Phe	Leu	Thr	Gly	Gln	Ala	Leu	Thr	260	265	270
Ser	Val	Leu	Asp	Leu	Leu	Phe	Ser	Phe	Ile	Phe	Phe	Ala	Val	Met	Trp	275	280	285
Tyr	Tyr	Ser	Pro	Lys	Leu	Thr	Leu	Val	Ile	Leu	Gly	Ser	Leu	Pro	Cys	290	295	300
Tyr	Ile	Leu	Trp	Ser	Ile	Phe	Ile	Ser	Pro	Ile	Leu	Arg	Arg	Arg	Leu	305	310	315
																		320

Asp Glu Lys Phe Ala Arg Ser Ala Asp Asn Gln Ala Phe Leu Val Glu
 325 330 335
 Ser Val Thr Ala Ile Asn Met Ile Lys Ala Met Ala Val Ala Pro Gln
 340 345 350
 Met Thr Asp Thr Trp Asp Lys Gln Leu Ala Ser Tyr Val Ser Ser Ser
 355 360 365
 Phe Arg Val Thr Val Leu Ala Thr Ile Gly Gln Gln Gly Val Gln Leu
 370 375 380
 Ile Gln Lys Thr Val Met Val Ile Asn Leu Trp Leu Gly Ala His Leu
 385 390 395 400
 Val Ile Ser Gly Asp Leu Ser Ile Gly Gln Leu Ile Ala Phe Asn Met
 405 410 415
 Leu Ser Gly Gln Val Ile Ala Pro Val Ile Arg Leu Ala Gln Leu Trp
 420 425 430
 Gln Asp Phe Gln Gln Val Gly Ile Ser Val Thr Arg Leu Gly Asp Val
 435 440 445
 Leu Asn Ser Pro Thr Glu Gln Tyr Gln Gly Lys Leu Ser Leu Pro Glu
 450 455 460
 Ile Lys Gly Asp Ile Ser Phe Lys Asn Ile Arg Phe Arg Tyr Lys Pro
 465 470 475 480
 Asp Ala Pro Thr Ile Leu Asn Asn Val Asn Leu Glu Ile Arg Gln Gly
 485 490 495
 Glu Val Ile Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu
 500 505 510
 Thr Lys Leu Leu Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu
 515 520 525
 Ile Asp Gly His Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg
 530 535 540
 Gln Ile Gly Val Val Leu Gln Asp Asn Val Leu Leu Asn Arg Ser Ile
 545 550 555 560
 Arg Glu Asn Ile Ala Leu Ser Asp Pro Gly Met Pro Met Glu Arg Val
 565 570 575
 Ile Tyr Ala Ala Lys Leu Ala Gly Ala His Asp Phe Ile Ser Glu Leu
 580 585 590
 Arg Glu Gly Tyr Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser
 595 600 605
 Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Asn Asn
 610 615 620

Pro Lys Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu
625 630 635 640

Ser Glu His Ile Ile Met Gln Asn Met Gln Lys Ile Cys Gln Gly Arg
645 650 655

Thr Val Ile Leu Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp
660 665 670

Arg Ile Ile Val Met Glu Lys Gly Glu Ile Val Glu Gln Gly Lys His
675 680 685

His Glu Leu Leu Gln Asn Ser Asn Gly Leu Tyr Ser Tyr Leu His Gln
690 695 700

Leu Gln Leu Asn
705

<210> 20

<211> 707

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 20

Met Asp Phe Tyr Arg Glu Glu Asp Tyr Gly Leu Tyr Ala Leu Thr Ile
1 5 10 15

Leu Ala Gln Tyr His Asn Ile Ala Val Asn Pro Glu Glu Leu Lys His
20 25 30

Lys Phe Asp Leu Glu Gly Lys Gly Leu Asp Leu Thr Ala Trp Leu Leu
35 40 45

Ala Ala Lys Ser Leu Glu Leu Lys Ala Lys Gln Val Lys Lys Ala Ile
50 55 60

Asp Arg Leu Ala Phe Ile Ala Leu Pro Ala Leu Val Trp Arg Glu Asp
65 70 75 80

Gly Lys His Phe Ile Leu Thr Lys Ile Asp Asn Glu Ala Lys Lys Tyr
85 90 95

Leu Ile Phe Asp Leu Glu Thr His Asn Pro Arg Ile Leu Glu Gln Ala
100 105 110

Glu Phe Glu Ser Leu Tyr Gln Gly Lys Leu Ile Leu Val Ala Ser Arg
115 120 125

Ala Ser Ile Val Gly Lys Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile
130 135 140

Pro Ala Val Ile Lys Tyr Arg Lys Ile Phe Ile Glu Thr Leu Ile Val
145 150 155 160

Ser Ile Phe Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln
165 170 175

Val	Val	Met	Asp	Lys	Val	Leu	Val	His	Arg	Gly	Phe	Ser	Thr	Leu	Asn	180	185	190
Val	Ile	Thr	Val	Ala	Leu	Ala	Ile	Val	Val	Leu	Phe	Glu	Ile	Val	Leu	195	200	205
Asn	Gly	Leu	Arg	Thr	Tyr	Ile	Phe	Ala	His	Ser	Thr	Ser	Arg	Ile	Asp	210	215	220
Val	Glu	Leu	Gly	Ala	Arg	Leu	Phe	Arg	His	Leu	Leu	Ala	Leu	Pro	Ile	225	230	235
Ser	Tyr	Phe	Glu	Asn	Arg	Arg	Val	Gly	Asp	Thr	Val	Ala	Arg	Val	Arg	245	250	255
Glu	Leu	Asp	Gln	Ile	Arg	Asn	Phe	Leu	Thr	Gly	Gln	Ala	Leu	Thr	Ser	260	265	270
Val	Leu	Asp	Leu	Met	Phe	Ser	Phe	Ile	Phe	Phe	Ala	Val	Met	Trp	Tyr	275	280	285
Tyr	Ser	Pro	Lys	Leu	Thr	Leu	Val	Ile	Leu	Gly	Ser	Leu	Pro	Phe	Tyr	290	295	300
Met	Gly	Trp	Ser	Ile	Phe	Ile	Ser	Pro	Ile	Leu	Arg	Arg	Arg	Leu	Asp	305	310	315
Glu	Lys	Phe	Ala	Arg	Gly	Ala	Asp	Asn	Gln	Ser	Phe	Leu	Val	Glu	Ser	325	330	335
Val	Thr	Ala	Ile	Asn	Thr	Ile	Lys	Ala	Leu	Ala	Val	Thr	Pro	Gln	Met	340	345	350
Thr	Asn	Thr	Trp	Asp	Lys	Gln	Leu	Ala	Ser	Tyr	Val	Ser	Ala	Gly	Phe	355	360	365
Arg	Val	Thr	Thr	Leu	Ala	Thr	Ile	Gly	Gln	Gln	Gly	Val	Gln	Phe	Ile	370	375	380
Gln	Lys	Val	Val	Met	Val	Ile	Thr	Leu	Trp	Leu	Gly	Ala	His	Leu	Val	385	390	395
Ile	Ser	Gly	Asp	Leu	Ser	Ile	Gly	Gln	Leu	Ile	Ala	Phe	Asn	Met	Leu	405	410	415
Ser	Gly	Gln	Val	Ile	Ala	Pro	Val	Ile	Arg	Leu	Ala	Gln	Leu	Trp	Gln	420	425	430
Asp	Phe	Gln	Gln	Val	Gly	Ile	Ser	Val	Thr	Arg	Leu	Gly	Asp	Val	Leu	435	440	445
Asn	Ser	Pro	Thr	Glu	Ser	Tyr	Gln	Gly	Lys	Leu	Ala	Leu	Pro	Glu	Ile	450	455	460
Lys	Gly	Asp	Ile	Thr	Phe	Arg	Asn	Ile	Arg	Phe	Arg	Tyr	Lys	Pro	Asp	465	470	475
																		480

Ala Pro Val Ile Leu Asn Asp Val Asn Leu Ser Ile Gln Gln Gly Glu
485 490 495

Val Ile Gly Ile Val Gly Arg Ser Gly Ser Gly Lys Ser Thr Leu Thr
500 505 510

Lys Leu Ile Gln Arg Phe Tyr Ile Pro Glu Asn Gly Gln Val Leu Ile
515 520 525

Asp Gly His Asp Leu Ala Leu Ala Asp Pro Asn Trp Leu Arg Arg Gln
530 535 540

Val Gly Val Val Leu Gln Asp Asn Val Leu Leu Asn Arg Ser Ile Arg
545 550 555 560

Asp Asn Ile Ala Leu Ala Asp Pro Gly Met Pro Met Glu Lys Ile Val
565 570 575

His Ala Ala Lys Leu Ala Gly Ala His Glu Phe Ile Ser Glu Leu Arg
580 585 590

Glu Gly Tyr Asn Thr Ile Val Gly Glu Gln Gly Ala Gly Leu Ser Gly
595 600 605

Gly Gln Arg Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Asn Asn Pro
610 615 620

Lys Ile Leu Ile Phe Asp Glu Ala Thr Ser Ala Leu Asp Tyr Glu Ser
625 630 635 640

Glu His Ile Ile Met Arg Asn Met His Gln Ile Cys Lys Gly Arg Thr
645 650 655

Val Ile Ile Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg
660 665 670

Ile Ile Val Met Glu Lys Gly Gln Ile Val Glu Gln Gly Lys His Lys
675 680 685

Glu Leu Leu Ala Asp Pro Asn Gly Leu Tyr His Tyr Leu His Gln Leu
690 695 700

Gln Ser Glu
705

<210> 21

<211> 707

<212> PRT

<213> Escherichia coli

<400> 21

Met Asp Ser Cys His Lys Ile Asp Tyr Gly Leu Tyr Ala Leu Glu Ile
1 5 10 15

Leu Ala Gln Tyr His Asn Val Ser Val Asn Pro Glu Glu Ile Lys His
20 25 30

Arg Phe Asp Thr Asp Gly Thr Gly Leu Gly Leu Thr Ser Trp Leu Leu
 35 40 45
 Ala Ala Lys Ser Leu Glu Leu Lys Val Lys Gln Val Lys Lys Thr Ile
 50 55 60
 Asp Arg Leu Asn Phe Ile Ser Leu Pro Ala Leu Val Trp Arg Glu Asp
 65 70 75 80
 Gly Arg His Phe Ile Leu Thr Lys Val Ser Lys Glu Ala Asn Arg Tyr
 85 90 95
 Leu Ile Phe Asp Leu Glu Gln Arg Asn Pro Arg Val Leu Glu Gln Ser
 100 105 110
 Glu Phe Glu Ala Leu Tyr Gln Gly His Ile Ile Leu Ile Ala Ser Arg
 115 120 125
 Ser Ser Val Ala Gly Lys Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile
 130 135 140
 Pro Ala Ile Ile Lys Tyr Arg Arg Ile Phe Ile Glu Thr Leu Val Val
 145 150 155 160
 Ser Val Phe Leu Gln Leu Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln
 165 170 175
 Val Val Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asn
 180 185 190
 Val Ile Thr Val Ala Leu Ser Val Val Val Val Phe Glu Ile Ile Leu
 195 200 205
 Ser Gly Leu Arg Thr Tyr Ile Phe Ala His Ser Thr Ser Arg Ile Asp
 210 215 220
 Val Glu Leu Gly Ala Lys Leu Phe Arg His Leu Leu Ala Leu Pro Ile
 225 230 235 240
 Ser Tyr Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Val Arg
 245 250 255
 Glu Leu Asp Gln Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser
 260 265 270
 Val Leu Asp Leu Leu Phe Ser Phe Ile Phe Phe Ala Val Met Trp Tyr
 275 280 285
 Tyr Ser Pro Lys Leu Thr Leu Val Ile Leu Phe Ser Leu Pro Cys Tyr
 290 295 300
 Ala Ala Trp Ser Val Phe Ile Ser Pro Ile Leu Arg Arg Arg Leu Asp
 305 310 315 320
 Asp Lys Phe Ser Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser
 325 330 335

Val	Thr	Ala	Ile	Asn	Thr	Ile	Lys	Ala	Met	Ala	Val	Ser	Pro	Gln	Met	340	345	350	
Thr	Asn	Ile	Trp	Asp	Lys	Gln	Leu	Ala	Gly	Tyr	Val	Ala	Ala	Gly	Phe	355	360	365	
Lys	Val	Thr	Val	Leu	Ala	Thr	Ile	Gly	Gln	Gln	Gly	Ile	Gln	Leu	Ile	370	375	380	
Gln	Lys	Thr	Val	Met	Ile	Ile	Asn	Leu	Trp	Leu	Gly	Ala	His	Leu	Val	385	390	395	400
Ile	Ser	Gly	Asp	Leu	Ser	Ile	Gly	Gln	Leu	Ile	Ala	Phe	Asn	Met	Leu	405	410	415	
Ala	Gly	Gln	Ile	Val	Ala	Pro	Val	Ile	Arg	Leu	Ala	Gln	Ile	Trp	Gln	420	425	430	
Asp	Phe	Gln	Gln	Val	Gly	Ile	Ser	Val	Thr	Arg	Leu	Gly	Asp	Val	Leu	435	440	445	
Asn	Ser	Pro	Thr	Glu	Ser	Tyr	His	Gly	Lys	Leu	Ala	Leu	Pro	Glu	Ile	450	455	460	
Asn	Gly	Asp	Ile	Thr	Phe	Arg	Asn	Ile	Arg	Phe	Arg	Tyr	Lys	Pro	Asp	465	470	475	480
Ser	Pro	Val	Ile	Leu	Asp	Asn	Ile	Asn	Leu	Ser	Ile	Lys	Gln	Gly	Glu	485	490	495	
Val	Ile	Gly	Ile	Val	Gly	Arg	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Thr	500	505	510	
Lys	Leu	Ile	Gln	Arg	Phe	Tyr	Ile	Pro	Glu	Asn	Gly	Gln	Val	Leu	Ile	515	520	525	
Asp	Gly	His	Asp	Leu	Ala	Leu	Ala	Asp	Pro	Asn	Trp	Leu	Arg	Arg	Gln	530	535	540	
Val	Gly	Val	Val	Leu	Gln	Asp	Asn	Val	Leu	Leu	Asn	Arg	Ser	Ile	Ile	545	550	555	560
Asp	Asn	Ile	Ser	Leu	Ala	Asn	Pro	Gly	Met	Ser	Val	Glu	Lys	Val	Ile	565	570	575	
Tyr	Ala	Ala	Lys	Leu	Ala	Gly	Ala	His	Asp	Phe	Ile	Ser	Glu	Leu	Arg	580	585	590	
Glu	Gly	Tyr	Asn	Thr	Ile	Val	Gly	Glu	Gln	Gly	Ala	Gly	Leu	Ser	Gly	595	600	605	
Gly	Gln	Arg	Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	Leu	Val	Asn	Asn	Pro	610	615	620	
Lys	Ile	Leu	Ile	Phe	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Tyr	Glu	Ser	625	630	635	640

Glu His Ile Ile Met Arg Asn Met His Lys Ile Cys Lys Gly Arg Thr
 645 650 655

Val Ile Ile Ile Ala His Arg Leu Ser Thr Val Lys Asn Ala Asp Arg
 660 665 670

Ile Ile Val Met Glu Lys Gly Lys Ile Val Glu Gln Gly Lys His Lys
 675 680 685

Glu Leu Leu Ser Glu Pro Glu Ser Leu Tyr Ser Tyr Leu Tyr Gln Leu
 690 695 700

Gln Ser Asp
 705

<210> 22
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
 aatgacgata tctttgttgg tcaaggtaaa

30

<210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (18)
 <223> a, t, c, g, other or unknown

<400> 23
 aayaaagart trgargcnga r

21

<210> 24
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
 <221> modified_base
 <222> (6)
 <223> a, t, c, g, other or unknown

<400> 24
ccytcnccrc trtgraadat rtcrtttraat tt

32

<210> 25
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (15)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (18)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (24)
<223> a, t, c, g, other or unknown

<400> 25
athgaytgga thgcncntt yggngay

27

<210> 26
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
actttatcca tcacracttg raaraa

26

<210> 27
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
gatcatatgt ccaatataaa tgtaattaa tctaa

35

<210> 28
<211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 28
 atcactagtt ccataatcta taaccaatga

30

<210> 29
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)..(2)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (5)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (7)
 <223> N or D

<220>
 <221> MOD_RES
 <222> (9)
 <223> Any amino acid

<400> 29
 Xaa Xaa Gly Gly Xaa Gly Xaa Asp Xaa
 1 5

<210> 30
 <211> 2215
 <212> DNA
 <213> Moraxella bovis

<220>
 <221> CDS
 <222> (1)..(2211)

<400> 30
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 Met Gly Gly Asp Thr Ser Leu Ile Arg Leu Asn Leu Gln Thr Leu Asn
 1 5 10 15

agt aat tta gtt atg ata gat tat gct caa caa cct gct cta tct gct	96
Ser Asn Leu Val Met Ile Asp Tyr Ala Gln Gln Pro Ala Leu Ser Ala	
20 25 30	
ctg gtt atc ctt gcc aaa tac tat ggt att tct gca agt cca gca gac	144
Leu Val Ile Leu Ala Lys Tyr Tyr Gly Ile Ser Ala Ser Pro Ala Asp	
35 40 45	
att atg cat cag ttt tct gat aat aca aaa gga gac ctg aat gaa att	192
Ile Met His Gln Phe Ser Asp Asn Thr Lys Gly Asp Leu Asn Glu Ile	
50 55 60	
gaa tgg atg ttg gca gca aag aaa tta gaa tta aag gta aag att ata	240
Glu Trp Met Leu Ala Ala Lys Lys Leu Glu Leu Lys Val Lys Ile Ile	
65 70 75 80	
aaa cag cct tta act cga ttg tca atg ata aca ctt cct gct ttg gtg	288
Lys Gln Pro Leu Thr Arg Leu Ser Met Ile Thr Leu Pro Ala Leu Val	
85 90 95	
tgg tgt gat aat aag ccc gat tta gat caa aat tta aac tct cat ttt	336
Trp Cys Asp Asn Lys Pro Asp Leu Asp Gln Asn Leu Asn Ser His Phe	
100 105 110	
ata cta act aaa att gat ggg gtg gga tct gct gca aaa tat ctc atc	384
Ile Leu Thr Lys Ile Asp Gly Val Gly Ser Ala Ala Lys Tyr Leu Ile	
115 120 125	
tac gat ttg att gag aat cgt ccc ata ata tta gat gca agt gag ttt	432
Tyr Asp Leu Ile Glu Asn Arg Pro Ile Ile Leu Asp Ala Ser Glu Phe	
130 135 140	
tct gaa aga tat tct ggt aag tta atg cta gta act tcc cgt gcg tca	480
Ser Glu Arg Tyr Ser Gly Lys Leu Met Leu Val Thr Ser Arg Ala Ser	
145 150 155 160	
ata ttg ggt tca ttg gct aaa ttt gat ttt act tgg ttt att cct gcg	528
Ile Leu Gly Ser Leu Ala Lys Phe Asp Phe Thr Trp Phe Ile Pro Ala	
165 170 175	
gta atc aaa tat cgt tat att ttt ttt gaa gtc atc gtt att tca gtg	576
Val Ile Lys Tyr Arg Tyr Ile Phe Phe Glu Val Ile Val Ile Ser Val	
180 185 190	
gtg cta cag att ttt gct ctg att acg cca ttg ttt ttt cag gtt gtg	624
Val Leu Gln Ile Phe Ala Leu Ile Thr Pro Leu Phe Phe Gln Val Val	
195 200 205	
atg gat aag gta ttg gtg cat cgt ggt ttt tct act ctg gat gtg gta	672
Met Asp Lys Val Leu Val His Arg Gly Phe Ser Thr Leu Asp Val Val	
210 215 220	
gcg att gcc ttg ttg gta gta agt tta ttt gaa gtc att tta agt ggt	720
Ala Ile Ala Leu Leu Val Val Ser Leu Phe Glu Val Ile Leu Ser Gly	
225 230 235 240	

cta cgc act tat att ttt gct cat aca acc tct cga att gat gta gag	768
Leu Arg Thr Tyr Ile Phe Ala His Thr Thr Ser Arg Ile Asp Val Glu	
245 250 255	
cta gga gca cga tta ttt cgt cat cta tta gct cta ccg ctt gct tat	816
Leu Gly Ala Arg Leu Phe Arg His Leu Leu Ala Leu Pro Leu Ala Tyr	
260 265 270	
ttt gag agt aga aga gta ggc gat aca gtt gca cgt ata cgt gaa ttg	864
Phe Glu Ser Arg Arg Val Gly Asp Thr Val Ala Arg Ile Arg Glu Leu	
275 280 285	
gaa cat atc cgc aat ttc tta act ggt caa gct ctc act tca gtt tta	912
Glu His Ile Arg Asn Phe Leu Thr Gly Gln Ala Leu Thr Ser Val Leu	
290 295 300	
gat ttg gtg ttt tct ttt ata ttc ttg ttt gta atg tgg tat tac agc	960
Asp Leu Val Phe Ser Phe Ile Phe Leu Phe Val Met Trp Tyr Tyr Ser	
305 310 315 320	
cct act tta aca ctg gta gtt ttg gca tca tta cca ata tat gcg ttt	1008
Pro Thr Leu Thr Leu Val Val Leu Ala Ser Leu Pro Ile Tyr Ala Phe	
325 330 335	
tgg tct gcc ttt att agc cca att tta cgc act cga cta aat gat caa	1056
Trp Ser Ala Phe Ile Ser Pro Ile Leu Arg Thr Arg Leu Asn Asp Gln	
340 345 350	
ttt gca cgc aat gca gat aat caa tct ttt tta gtg gaa agt att act	1104
Phe Ala Arg Asn Ala Asp Asn Gln Ser Phe Leu Val Glu Ser Ile Thr	
355 360 365	
gcg gtt ggt acg gta aaa gca atg gca gtt gaa cct caa atg acc cgt	1152
Ala Val Gly Thr Val Lys Ala Met Ala Val Glu Pro Gln Met Thr Arg	
370 375 380	
cgc tgg gat aat caa tta gca gct tat gtg gtt tct agt ttt cgg gta	1200
Arg Trp Asp Asn Gln Leu Ala Ala Tyr Val Val Ser Ser Phe Arg Val	
385 390 395 400	
gct aag ttg gca atg gtt ggg cag caa gga gta caa ctc att caa aag	1248
Ala Lys Leu Ala Met Val Gly Gln Gln Gly Val Gln Leu Ile Gln Lys	
405 410 415	
atg gtt att gtg gca act cta tgg att ggt gca aaa ttg gta att gaa	1296
Met Val Ile Val Ala Thr Leu Trp Ile Gly Ala Lys Leu Val Ile Glu	
420 425 430	
ggc aag cta tcg gta ggt caa tta ata gca ttt aat atg ctg gca ggt	1344
Gly Lys Leu Ser Val Gly Gln Leu Ile Ala Phe Asn Met Leu Ala Gly	
435 440 445	
cag gtg gcc gct cct gtt atc cgc ctg gca cag cta tgg caa gat ttt	1392
Gln Val Ala Ala Pro Val Ile Arg Leu Ala Gln Leu Trp Gln Asp Phe	
450 455 460	

cag	caa	gta	ggg	att	tca	gtg	gcg	aga	ttg	ggg	gat	att	tta	aat	act	1440
Gln	Gln	Val	Gly	Ile	Ser	Val	Ala	Arg	Leu	Gly	Asp	Ile	Leu	Asn	Thr	
465					470					475					480	
cca	act	gag	cat	tct	aca	tct	cgc	tta	act	tta	cct	gat	att	aag	ggg	1488
Pro	Thr	Glu	His	Ser	Thr	Ser	Arg	Leu	Thr	Leu	Pro	Asp	Ile	Lys	Gly	
				485					490					495		
gat	att	aca	ttt	gaa	aat	gtt	gat	ttt	cgc	tac	aaa	ata	gat	ggg	cat	1536
Asp	Ile	Thr	Phe	Glu	Asn	Val	Asp	Phe	Arg	Tyr	Lys	Ile	Asp	Gly	His	
			500					505					510			
tta	ata	tta	cag	aat	tta	aat	tta	cag	att	aac	gct	gga	gag	ata	cta	1584
Leu	Ile	Leu	Gln	Asn	Leu	Asn	Leu	Gln	Ile	Asn	Ala	Gly	Glu	Ile	Leu	
		515					520					525				
ggg	atc	gta	gga	cgc	tct	ggg	tca	ggg	aaa	tca	aca	ttg	aca	aaa	tta	1632
Gly	Ile	Val	Gly	Arg	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Thr	Lys	Leu	
	530					535				540						
gta	cag	cgt	tta	tat	gta	cca	gaa	aat	ggg	cga	ata	tta	gtt	gat	gga	1680
Val	Gln	Arg	Leu	Tyr	Val	Pro	Glu	Asn	Gly	Arg	Ile	Leu	Val	Asp	Gly	
545					550					555					560	
aac	gat	ttg	gca	tta	gct	gat	ccc	gct	tgg	ctg	cgt	cgc	caa	gtg	ggg	1728
Asn	Asp	Leu	Ala	Leu	Ala	Asp	Pro	Ala	Trp	Leu	Arg	Arg	Gln	Val	Gly	
			565					570						575		
gtt	gtt	ttg	cag	gaa	aat	gtg	tta	ctc	aat	cgt	agt	att	cga	gat	aat	1776
Val	Val	Leu	Gln	Glu	Asn	Val	Leu	Leu	Asn	Arg	Ser	Ile	Arg	Asp	Asn	
		580					585						590			
att	gcc	cta	act	gat	acg	ggc	atg	tca	tta	gag	ttt	att	atc	cag	gct	1824
Ile	Ala	Leu	Thr	Asp	Thr	Gly	Met	Ser	Leu	Glu	Phe	Ile	Ile	Gln	Ala	
		595					600						605			
gcc	aag	atg	tct	ggg	gca	cat	gac	ttt	att	atg	gaa	ttg	cct	gag	ggg	1872
Ala	Lys	Met	Ser	Gly	Ala	His	Asp	Phe	Ile	Met	Glu	Leu	Pro	Glu	Gly	
	610					615					620					
tat	gat	acg	att	gtt	gga	gag	caa	ggg	gca	ggc	ttg	tca	ggg	gga	caa	1920
Tyr	Asp	Thr	Ile	Val	Gly	Glu	Gln	Gly	Ala	Gly	Leu	Ser	Gly	Gly	Gln	
625					630					635					640	
cgc	cag	cgt	atc	gct	att	gcg	cgt	gct	tta	att	acc	aat	ccg	cgt	att	1968
Arg	Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	Leu	Ile	Thr	Asn	Pro	Arg	Ile	
				645					650					655		
ttg	att	ttt	gat	gaa	gct	act	agt	gca	tta	gac	tat	gag	tcg	gaa	agg	2016
Leu	Ile	Phe	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Tyr	Glu	Ser	Glu	Arg	
		660						665					670			
gct	att	atg	caa	aat	atg	cag	gca	att	tgc	caa	ggg	aga	aca	gtg	ttg	2064
Ala	Ile	Met	Gln	Asn	Met	Gln	Ala	Ile	Cys	Gln	Gly	Arg	Thr	Val	Leu	
		675					680					685				

att att gca cat cgc tta tct acc gta aaa atg gca cat cgc att att 2112
 Ile Ile Ala His Arg Leu Ser Thr Val Lys Met Ala His Arg Ile Ile
 690 695 700

gca atg gac aag ggg aaa att gta gag caa ggc aca cat caa gaa ttg 2160
 Ala Met Asp Lys Gly Lys Ile Val Glu Gln Gly Thr His Gln Glu Leu
 705 710 715 720

ttg caa aaa gaa gat ggt tac tat cgt tat tta tat gat ttg cag aat 2208
 Leu Gln Lys Glu Asp Gly Tyr Tyr Arg Tyr Leu Tyr Asp Leu Gln Asn
 725 730 735

gga taaa 2215
 Gly

<210> 31

<211> 507

<212> DNA

<213> Moraxella bovis

<220>

<221> CDS

<222> (1)..(504)

<400> 31

atg acg aaa aag ttt gca gag cta ggt tta att gca tgg ctt tgg tct 48
 Met Thr Lys Lys Phe Ala Glu Leu Gly Leu Ile Ala Trp Leu Trp Ser
 1 5 10 15

aac tct gat atg cat aaa cat tgg acg ttg tct ttg ttt gcg acc aat 96
 Asn Ser Asp Met His Lys His Trp Thr Leu Ser Leu Phe Ala Thr Asn
 20 25 30

gtt att ccg gca att gag aca ggt caa tat gtt ata ttg aaa aga gaa 144
 Val Ile Pro Ala Ile Glu Thr Gly Gln Tyr Val Ile Leu Lys Arg Glu
 35 40 45

gat atg cct gta gca tat tgt agt tgg gct aaa ctt agt tta gaa aac 192
 Asp Met Pro Val Ala Tyr Cys Ser Trp Ala Lys Leu Ser Leu Glu Asn
 50 55 60

gag gtt aaa tat att aac gat gtt act tct ctt aag tta gat gac tgg 240
 Glu Val Lys Tyr Ile Asn Asp Val Thr Ser Leu Lys Leu Asp Asp Trp
 65 70 75 80

cag tca ggt gac cga aac tgg ttt att gac tgg att gct cca ttt ggc 288
 Gln Ser Gly Asp Arg Asn Trp Phe Ile Asp Trp Ile Ala Pro Phe Gly
 85 90 95

gat agt ctt aca ctc aca aaa cac atg aga acg tta ttt tca gat gaa 336
 Asp Ser Leu Thr Leu Thr Lys His Met Arg Thr Leu Phe Ser Asp Glu
 100 105 110

ttg ttt aga gcg att cgt gta gat gga aat tca tcg cat ggt aag ata 384
 Leu Phe Arg Ala Ile Arg Val Asp Gly Asn Ser Ser His Gly Lys Ile
 115 120 125

tct gaa ttt tat gga aag tct gtt gat tca aaa tta gcc tca aga ata 432
 Ser Glu Phe Tyr Gly Lys Ser Val Asp Ser Lys Leu Ala Ser Arg Ile
 130 135 140

ttt gca caa tat cac gaa gat ttg acg agc aaa ttg tca act cag aat 480
 Phe Ala Gln Tyr His Glu Asp Leu Thr Ser Lys Leu Ser Thr Gln Asn
 145 150 155 160

aat ttt att ata tct aaa gat aat taa 507
 Asn Phe Ile Ile Ser Lys Asp Asn
 165

<210> 32
 <211> 168
 <212> PRT
 <213> Moraxella bovis

<400> 32
 Met Thr Lys Lys Phe Ala Glu Leu Gly Leu Ile Ala Trp Leu Trp Ser
 1 5 10 15

Asn Ser Asp Met His Lys His Trp Thr Leu Ser Leu Phe Ala Thr Asn
 20 25 30

Val Ile Pro Ala Ile Glu Thr Gly Gln Tyr Val Ile Leu Lys Arg Glu
 35 40 45

Asp Met Pro Val Ala Tyr Cys Ser Trp Ala Lys Leu Ser Leu Glu Asn
 50 55 60

Glu Val Lys Tyr Ile Asn Asp Val Thr Ser Leu Lys Leu Asp Asp Trp
 65 70 75 80

Gln Ser Gly Asp Arg Asn Trp Phe Ile Asp Trp Ile Ala Pro Phe Gly
 85 90 95

Asp Ser Leu Thr Leu Thr Lys His Met Arg Thr Leu Phe Ser Asp Glu
 100 105 110

Leu Phe Arg Ala Ile Arg Val Asp Gly Asn Ser Ser His Gly Lys Ile
 115 120 125

Ser Glu Phe Tyr Gly Lys Ser Val Asp Ser Lys Leu Ala Ser Arg Ile
 130 135 140

Phe Ala Gln Tyr His Glu Asp Leu Thr Ser Lys Leu Ser Thr Gln Asn
 145 150 155 160

Asn Phe Ile Ile Ser Lys Asp Asn
 165

<210> 33
 <211> 167
 <212> PRT
 <213> Pasteurella haemolytica

<400> 33

Met	Asn	Gln	Ser	Tyr	Phe	Asn	Leu	Leu	Gly	Asn	Ile	Thr	Trp	Leu	Trp
1				5					10					15	
Met	Asn	Ser	Ser	Leu	His	Lys	Glu	Trp	Ser	Cys	Glu	Leu	Leu	Ala	Arg
			20					25					30		
Asn	Val	Ile	Pro	Ala	Ile	Glu	Asn	Glu	Gln	Tyr	Met	Leu	Leu	Ile	Asp
		35					40					45			
Asn	Gly	Ile	Pro	Ile	Ala	Tyr	Cys	Ser	Trp	Ala	Asp	Leu	Asn	Leu	Glu
	50					55					60				
Thr	Glu	Val	Lys	Tyr	Ile	Lys	Asp	Ile	Asn	Ser	Leu	Thr	Pro	Glu	Glu
65					70					75				80	
Trp	Gln	Ser	Gly	Asp	Arg	Arg	Trp	Ile	Ile	Asp	Trp	Val	Ala	Pro	Phe
				85					90					95	
Gly	His	Ser	Gln	Leu	Leu	Tyr	Lys	Lys	Met	Cys	Gln	Lys	Tyr	Pro	Asp
			100					105					110		
Met	Ile	Val	Arg	Ser	Ile	Arg	Phe	Tyr	Pro	Lys	Gln	Lys	Glu	Leu	Gly
	115						120					125			
Lys	Ile	Ala	Tyr	Phe	Lys	Gly	Gly	Lys	Leu	Asp	Lys	Lys	Thr	Ala	Lys
	130					135					140				
Lys	Arg	Phe	Asp	Thr	Tyr	Gln	Glu	Glu	Leu	Ala	Thr	Ala	Leu	Lys	Asn
145					150				155					160	
Glu	Phe	Asn	Phe	Ile	Lys	Lys									
				165											

<210> 34

<211> 172

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 34

Met	Ser	Lys	Lys	Ile	Asn	Gly	Phe	Glu	Val	Leu	Gly	Glu	Val	Ala	Trp
1				5					10					15	
Leu	Trp	Ala	Ser	Ser	Pro	Leu	His	Arg	Lys	Trp	Pro	Leu	Ser	Leu	Leu
			20					25					30		
Ala	Ile	Asn	Val	Leu	Pro	Ala	Ile	Glu	Ser	Asn	Gln	Tyr	Val	Leu	Leu
		35					40					45			
Lys	Arg	Asp	Gly	Phe	Pro	Ile	Ala	Phe	Cys	Ser	Trp	Ala	Asn	Leu	Asn
	50					55					60				
Leu	Glu	Asn	Glu	Ile	Lys	Tyr	Leu	Asp	Asp	Val	Ala	Ser	Leu	Val	Ala
65					70					75				80	

Asp Asp Trp Thr Ser Gly Asp Arg Arg Trp Phe Ile Asp Trp Ile Ala
 85 90 95
 Pro Phe Gly Asp Ser Ala Ala Leu Tyr Lys His Met Arg Asp Asn Phe
 100 105 110
 Pro Asn Glu Leu Phe Arg Ala Ile Arg Val Asp Pro Asp Ser Arg Val
 115 120 125
 Gly Lys Ile Ser Glu Phe His Gly Gly Lys Ile Asp Lys Lys Leu Ala
 130 135 140
 Ser Lys Ile Phe Gln Gln Tyr His Phe Glu Leu Met Ser Glu Leu Lys
 145 150 155 160
 Asn Lys Gln Asn Phe Lys Phe Ser Leu Val Asn Ser
 165 170

<210> 35
 <211> 170
 <212> PRT
 <213> Escherichia coli

<400> 35
 Met Asn Arg Asn Asn Pro Leu Glu Val Leu Gly His Val Ser Trp Leu
 1 5 10 15
 Trp Ala Ser Ser Pro Leu His Arg Asn Trp Pro Val Ser Leu Phe Ala
 20 25 30
 Ile Asn Val Leu Pro Ala Ile Arg Ala Asn Gln Tyr Ala Leu Leu Thr
 35 40 45
 Arg Asp Asn Tyr Pro Val Ala Tyr Cys Ser Trp Ala Asn Leu Ser Leu
 50 55 60
 Glu Asn Glu Ile Lys Tyr Leu Asn Asp Val Thr Ser Leu Val Ala Glu
 65 70 75 80
 Asp Trp Thr Ser Gly Asp Arg Lys Trp Phe Ile Val Trp Ile Ala Pro
 85 90 95
 Phe Gly Asp Asn Gly Ala Leu Tyr Lys Tyr Met Arg Lys Lys Phe Pro
 100 105 110
 Asp Glu Leu Phe Arg Ala Ile Arg Val Asp Pro Lys Thr His Val Gly
 115 120 125
 Lys Val Ser Glu Phe His Gly Gly Lys Ile Asp Lys Gln Leu Ala Asn
 130 135 140
 Lys Ile Phe Lys Gln Tyr His His Glu Leu Ile Thr Glu Val Lys Asn
 145 150 155 160
 Lys Ser Asp Phe Asn Phe Ser Leu Thr Gly
 165 170

<210> 36
 <211> 1428
 <212> DNA
 <213> Moraxella bovis

<220>
 <221> CDS
 <222> (1)..(1425)

<400> 36
 atg ttt ata caa gca ctt aaa gat ttt ttt att cgc tat ata acc gtt 48
 Met Phe Ile Gln Ala Leu Lys Asp Phe Phe Ile Arg Tyr Ile Thr Val
 1 5 10 15

tgg cgc aat aca tgg gca gtt cga gac caa cta acc cct cct aag cgt 96
 Trp Arg Asn Thr Trp Ala Val Arg Asp Gln Leu Thr Pro Pro Lys Arg
 20 25 30

act aaa gaa gaa ctc gct ttt ctt cct gca cat cta gaa ctc act gac 144
 Thr Lys Glu Glu Leu Ala Phe Leu Pro Ala His Leu Glu Leu Thr Asp
 35 40 45

aca cct gta tcc aga tct tct aag tgg aca gct aga ata atc atg ata 192
 Thr Pro Val Ser Arg Ser Ser Lys Trp Thr Ala Arg Ile Ile Met Ile
 50 55 60

ttt gtc cta ttt gct ttg cta tgg tct tgg gtt gga cag att gac att 240
 Phe Val Leu Phe Ala Leu Leu Trp Ser Trp Val Gly Gln Ile Asp Ile
 65 70 75 80

gtt gct aca gct tca ggt aaa att tct tca ggt agc cgt agc aag act 288
 Val Ala Thr Ala Ser Gly Lys Ile Ser Ser Gly Ser Arg Ser Lys Thr
 85 90 95

att caa tct ttg gaa aca gcg ata gtt aaa gca gtt tat gta cgt gat 336
 Ile Gln Ser Leu Glu Thr Ala Ile Val Lys Ala Val Tyr Val Arg Asp
 100 105 110

ggt caa aat gtt caa caa ggt gaa ata tta gta gat tta gtg gga atc 384
 Gly Gln Asn Val Gln Gln Gly Glu Ile Leu Val Asp Leu Val Gly Ile
 115 120 125

ggt tca gat agt gat gtt gct cag tcc gag aaa gcc ctt cga gca gcg 432
 Gly Ser Asp Ser Asp Val Ala Gln Ser Glu Lys Ala Leu Arg Ala Ala
 130 135 140

caa tta tct aag cta cgc ctt gaa gca att tta tca gca tta aat cac 480
 Gln Leu Ser Lys Leu Arg Leu Glu Ala Ile Leu Ser Ala Leu Asn His
 145 150 155 160

cgt att aat cct cag att gat gta gca tat gca aag tct tta aat att 528
 Arg Ile Asn Pro Gln Ile Asp Val Ala Tyr Ala Lys Ser Leu Asn Ile
 165 170 175

tca gaa tcg gaa att aat gaa gct caa act tta gcc caa aat caa tat 576
 Ser Glu Ser Glu Ile Asn Glu Ala Gln Thr Leu Ala Gln Asn Gln Tyr
 180 185 190

caa gca tgg tta gca caa gat gaa caa cta aaa tta acc tta aaa gga	624
Gln Ala Trp Leu Ala Gln Asp Glu Gln Leu Lys Leu Thr Leu Lys Gly	
195 200 205	
cat caa gca gaa tta caa tct gct cga tcc caa gaa caa aag ttg gtt	672
His Gln Ala Glu Leu Gln Ser Ala Arg Ser Gln Glu Gln Lys Leu Val	
210 215 220	
tca gtt ggt gca att gaa cat caa aag act gat gat tat cgg agt ctc	720
Ser Val Gly Ala Ile Glu His Gln Lys Thr Asp Asp Tyr Arg Ser Leu	
225 230 235 240	
aaa gca gaa aat ttt ata tct gag cat gct tat cta gaa caa gaa agc	768
Lys Ala Glu Asn Phe Ile Ser Glu His Ala Tyr Leu Glu Gln Glu Ser	
245 250 255	
aaa tta ctt agc aat caa aat gat tta caa agt aca cgt agt cag att	816
Lys Leu Leu Ser Asn Gln Asn Asp Leu Gln Ser Thr Arg Ser Gln Ile	
260 265 270	
caa aaa ata cag gct gca atc atg caa gct gaa cag aac cgt atg tta	864
Gln Lys Ile Gln Ala Ala Ile Met Gln Ala Glu Gln Asn Arg Met Leu	
275 280 285	
tat act caa aat cta aaa cgt gat aca tta gaa tct tta cgc caa acc	912
Tyr Thr Gln Asn Leu Lys Arg Asp Thr Leu Glu Ser Leu Arg Gln Thr	
290 295 300	
aat gaa cag att aat caa tat act ggt caa act aat aaa gct aag cag	960
Asn Glu Gln Ile Asn Gln Tyr Thr Gly Gln Thr Asn Lys Ala Lys Gln	
305 310 315 320	
cga cag aaa ttg ctg agt att aaa tca cct gtt aat ggt act ata caa	1008
Arg Gln Lys Leu Leu Ser Ile Lys Ser Pro Val Asn Gly Thr Ile Gln	
325 330 335	
gag cta aca gct tat act tta ggt gga gtt gta caa gca gca caa aaa	1056
Glu Leu Thr Ala Tyr Thr Leu Gly Gly Val Val Gln Ala Ala Gln Lys	
340 345 350	
att atg gtt gtg gca cct aac gat aat caa gtg gaa gta gag gta tta	1104
Ile Met Val Val Ala Pro Asn Asp Asn Gln Val Glu Val Glu Val Leu	
355 360 365	
gtg cta aat aaa gat atc ggc ttt gta aaa gct ggg cag aat gtt atc	1152
Val Leu Asn Lys Asp Ile Gly Phe Val Lys Ala Gly Gln Asn Val Ile	
370 375 380	
atc aaa atc gag agt ttt cct tat aca cgt tat ggt tat tta aca ggt	1200
Ile Lys Ile Glu Ser Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu Thr Gly	
385 390 395 400	
aaa ata aaa agt att agt cat gat gct ata gaa cat caa cat tta ggt	1248
Lys Ile Lys Ser Ile Ser His Asp Ala Ile Glu His Gln His Leu Gly	
405 410 415	

cta gtg tat act gca ctt gtt tct ctt gat aaa agc aca tta aat ata 1296
 Leu Val Tyr Thr Ala Leu Val Ser Leu Asp Lys Ser Thr Leu Asn Ile
 420 425 430

gat gga gta aca atc aac tta acg cca gga atg aat gtt act gct gaa 1344
 Asp Gly Val Thr Ile Asn Leu Thr Pro Gly Met Asn Val Thr Ala Glu
 435 440 445

att aaa aca ggt aaa cgt cgt gtt ttg gat tat ata tta agt cca ttg 1392
 Ile Lys Thr Gly Lys Arg Arg Val Leu Asp Tyr Ile Leu Ser Pro Leu
 450 455 460

cag aca aaa gtt gat gaa agt ttt cga gaa cgc taa 1428
 Gln Thr Lys Val Asp Glu Ser Phe Arg Glu Arg
 465 470 475

<210> 37

<211> 475

<212> PRT

<213> Moraxella bovis

<400> 37

Met Phe Ile Gln Ala Leu Lys Asp Phe Phe Ile Arg Tyr Ile Thr Val
 1 5 10 15

Trp Arg Asn Thr Trp Ala Val Arg Asp Gln Leu Thr Pro Pro Lys Arg
 20 25 30

Thr Lys Glu Glu Leu Ala Phe Leu Pro Ala His Leu Glu Leu Thr Asp
 35 40 45

Thr Pro Val Ser Arg Ser Ser Lys Trp Thr Ala Arg Ile Ile Met Ile
 50 55 60

Phe Val Leu Phe Ala Leu Leu Trp Ser Trp Val Gly Gln Ile Asp Ile
 65 70 75 80

Val Ala Thr Ala Ser Gly Lys Ile Ser Ser Gly Ser Arg Ser Lys Thr
 85 90 95

Ile Gln Ser Leu Glu Thr Ala Ile Val Lys Ala Val Tyr Val Arg Asp
 100 105 110

Gly Gln Asn Val Gln Gln Gly Glu Ile Leu Val Asp Leu Val Gly Ile
 115 120 125

Gly Ser Asp Ser Asp Val Ala Gln Ser Glu Lys Ala Leu Arg Ala Ala
 130 135 140

Gln Leu Ser Lys Leu Arg Leu Glu Ala Ile Leu Ser Ala Leu Asn His
 145 150 155 160

Arg Ile Asn Pro Gln Ile Asp Val Ala Tyr Ala Lys Ser Leu Asn Ile
 165 170 175

Ser Glu Ser Glu Ile Asn Glu Ala Gln Thr Leu Ala Gln Asn Gln Tyr
 180 185 190

Gln Ala Trp Leu Ala Gln Asp Glu Gln Leu Lys Leu Thr Leu Lys Gly
 195 200 205
 His Gln Ala Glu Leu Gln Ser Ala Arg Ser Gln Glu Gln Lys Leu Val
 210 215 220
 Ser Val Gly Ala Ile Glu His Gln Lys Thr Asp Asp Tyr Arg Ser Leu
 225 230 235 240
 Lys Ala Glu Asn Phe Ile Ser Glu His Ala Tyr Leu Glu Gln Glu Ser
 245 250 255
 Lys Leu Leu Ser Asn Gln Asn Asp Leu Gln Ser Thr Arg Ser Gln Ile
 260 265 270
 Gln Lys Ile Gln Ala Ala Ile Met Gln Ala Glu Gln Asn Arg Met Leu
 275 280 285
 Tyr Thr Gln Asn Leu Lys Arg Asp Thr Leu Glu Ser Leu Arg Gln Thr
 290 295 300
 Asn Glu Gln Ile Asn Gln Tyr Thr Gly Gln Thr Asn Lys Ala Lys Gln
 305 310 315 320
 Arg Gln Lys Leu Leu Ser Ile Lys Ser Pro Val Asn Gly Thr Ile Gln
 325 330 335
 Glu Leu Thr Ala Tyr Thr Leu Gly Gly Val Val Gln Ala Ala Gln Lys
 340 345 350
 Ile Met Val Val Ala Pro Asn Asp Asn Gln Val Glu Val Glu Val Leu
 355 360 365
 Val Leu Asn Lys Asp Ile Gly Phe Val Lys Ala Gly Gln Asn Val Ile
 370 375 380
 Ile Lys Ile Glu Ser Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu Thr Gly
 385 390 395 400
 Lys Ile Lys Ser Ile Ser His Asp Ala Ile Glu His Gln His Leu Gly
 405 410 415
 Leu Val Tyr Thr Ala Leu Val Ser Leu Asp Lys Ser Thr Leu Asn Ile
 420 425 430
 Asp Gly Val Thr Ile Asn Leu Thr Pro Gly Met Asn Val Thr Ala Glu
 435 440 445
 Ile Lys Thr Gly Lys Arg Arg Val Leu Asp Tyr Ile Leu Ser Pro Leu
 450 455 460
 Gln Thr Lys Val Asp Glu Ser Phe Arg Glu Arg
 465 470 475

<210> 38
 <211> 478
 <212> PRT
 <213> *Pasteurella haemolytica*

<400> 38

Met	Lys	Ile	Trp	Leu	Ser	Gly	Ile	Tyr	Glu	Phe	Phe	Leu	Arg	Tyr	Lys	1	5	10	15
Asn	Ile	Trp	Ala	Glu	Val	Trp	Lys	Ile	Arg	Lys	Glu	Leu	Asp	His	Pro	20	25	30	
Asn	Arg	Lys	Lys	Asp	Glu	Ser	Glu	Phe	Leu	Pro	Ala	His	Leu	Glu	Leu	35	40	45	
Ile	Glu	Thr	Pro	Val	Ser	Lys	Lys	Pro	Arg	Leu	Ile	Ala	Tyr	Leu	Ile	50	55	60	
Met	Leu	Phe	Leu	Val	Val	Ala	Ile	Val	Leu	Ala	Ser	Val	Ser	Lys	Val	65	70	75	80
Glu	Ile	Val	Ala	Thr	Ala	Pro	Gly	Lys	Leu	Thr	Phe	Ser	Gly	Arg	Ser	85	90	95	
Lys	Glu	Ile	Lys	Pro	Ile	Glu	Asn	Ala	Ile	Val	Gln	Glu	Ile	Phe	Val	100	105	110	
Lys	Asp	Gly	Gln	Phe	Val	Glu	Lys	Gly	Gln	Leu	Leu	Val	Ser	Leu	Thr	115	120	125	
Ala	Leu	Gly	Ser	Asp	Ala	Asp	Ile	Lys	Lys	Thr	Met	Ala	Ser	Leu	Ser	130	135	140	
Leu	Ala	Lys	Leu	Glu	Asn	Tyr	Arg	Tyr	Gln	Thr	Leu	Leu	Thr	Ala	Ile	145	150	155	160
Glu	Lys	Glu	Ser	Leu	Pro	Val	Ile	Asp	Leu	Ser	Arg	Thr	Glu	Phe	Lys	165	170	175	
Asp	Ser	Ser	Glu	Glu	Asp	Arg	Leu	Arg	Ile	Lys	His	Leu	Ile	Glu	Glu	180	185	190	
Gln	Tyr	Thr	Thr	Trp	Gln	Lys	Gln	Lys	Thr	Gln	Lys	Thr	Leu	Ala	Tyr	195	200	205	
Lys	Arg	Lys	Glu	Ala	Glu	Lys	Gln	Thr	Ile	Phe	Ala	Tyr	Val	Arg	Lys	210	215	220	
Tyr	Glu	Gly	Ala	Thr	Arg	Ile	Glu	Gln	Glu	Lys	Leu	Lys	Asp	Phe	Lys	225	230	235	240
Ala	Leu	Tyr	Lys	Gln	Lys	Ser	Leu	Ser	Lys	His	Glu	Leu	Leu	Ala	Gln	245	250	255	
Glu	Asn	Lys	Leu	Ile	Glu	Ala	Gln	Asn	Ala	Val	Ala	Val	Tyr	Arg	Ser	260	265	270	

Lys Leu Asn Glu Leu Glu Asn Asp Leu Leu Asn Val Lys Glu Glu Leu
275 280 285

Glu Leu Ile Thr Gln Phe Phe Lys Ser Asp Val Leu Glu Lys Leu Lys
290 295 300

Gln His Ile Glu Asn Glu Arg Gln Leu Arg Leu Glu Leu Glu Lys Asn
305 310 315 320

Asn Gln Arg Arg Gln Ala Ser Met Ile Arg Ala Pro Val Ser Gly Thr
325 330 335

Val Gln Gln Leu Lys Ile His Thr Ile Gly Gly Val Val Thr Thr Ala
340 345 350

Glu Thr Leu Met Ile Ile Val Pro Glu Asp Asp Val Leu Glu Ala Thr
355 360 365

Ala Leu Val Pro Asn Lys Asp Ile Gly Phe Val Ala Ala Gly Gln Glu
370 375 380

Val Ile Ile Lys Val Glu Thr Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu
385 390 395 400

Thr Gly Arg Ile Lys His Ile Ser Pro Asp Ala Ile Glu Gln Pro Asn
405 410 415

Val Gly Leu Val Phe Asn Ala Thr Ile Ala Ile Asp Arg Lys Asn Leu
420 425 430

Thr Ser Pro Asp Gly Arg Lys Ile Asp Leu Ser Ser Gly Met Thr Ile
435 440 445

Thr Ala Glu Ile Lys Thr Gly Glu Arg Ser Val Met Ser Tyr Leu Leu
450 455 460

Ser Pro Leu Glu Glu Ser Val Thr Glu Ser Leu Arg Glu Arg
465 470 475

<210> 39

<211> 478

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 39

Met Lys Thr Trp Leu Met Gly Leu Tyr Glu Phe Phe Gln Arg Tyr Lys
1 5 10 15

Thr Val Trp Thr Glu Ile Trp Lys Ile Arg His Gln Leu Asp Thr Pro
20 25 30

Asp Arg Glu Lys Asp Glu Asn Glu Phe Leu Pro Ala His Leu Glu Leu
35 40 45

Ile Glu Thr Pro Val Ser Lys Lys Pro Arg Leu Ile Ala Tyr Leu Ile
50 55 60

Met	Leu	Phe	Leu	Phe	Leu	Ala	Leu	Val	Ile	Ser	Ile	Val	Ser	His	Val	65	70	75	80
Glu	Ile	Val	Ala	Thr	Ala	Thr	Gly	Lys	Leu	Ala	Phe	Ser	Asp	Arg	Ser	85	90	95	
Lys	Glu	Ile	Lys	Pro	Ile	Glu	Asn	Ala	Leu	Val	Lys	Glu	Ile	Phe	Val	100	105	110	
Gln	Asp	Gly	Gln	Phe	Val	Glu	Lys	Asp	Gln	Leu	Leu	Leu	His	Leu	Thr	115	120	125	
Ala	Leu	Gly	Ala	Asp	Ala	Asp	Gln	Gln	Lys	Thr	Lys	Ser	Ser	Leu	Ser	130	135	140	
Leu	Thr	Lys	Leu	Glu	Arg	Tyr	Arg	Tyr	Glu	Ile	Leu	Leu	Glu	Ala	Val	145	150	155	160
Ala	Ala	Asp	Arg	Leu	Pro	Leu	Ile	Glu	Leu	Thr	Lys	Asp	Glu	Phe	Lys	165	170	175	
His	Ala	Thr	Glu	Glu	Asp	Lys	Thr	Arg	Ile	Arg	Tyr	Leu	Ile	Thr	Glu	180	185	190	
Gln	Phe	Glu	Ala	Trp	Gln	Lys	Gln	Lys	Tyr	Gln	Lys	Glu	Leu	Ala	Leu	195	200	205	
Gln	Arg	Arg	Glu	Ala	Glu	Lys	Gln	Thr	Val	Leu	Ala	Asn	Ile	Arg	Lys	210	215	220	
Tyr	Glu	Gly	Ile	Ser	Arg	Val	Glu	Asn	Glu	Arg	Leu	Lys	Asp	Leu	Lys	225	230	235	240
Lys	Leu	Phe	Asn	Ser	Lys	Ser	Thr	Ser	Lys	His	Asp	Val	Leu	Thr	Gln	245	250	255	
Glu	Asn	Arg	His	Ile	Glu	Ala	Val	Asn	Glu	Leu	Ala	Val	Tyr	Lys	Ser	260	265	270	
Arg	Leu	Asn	Glu	Val	Glu	Ser	Asp	Leu	Arg	Gln	Ala	Lys	Glu	Glu	Ile	275	280	285	
His	Leu	Ile	Thr	Gln	Leu	Phe	Arg	Ala	Asp	Ile	Leu	Glu	Lys	Leu	Lys	290	295	300	
Gln	Asn	Val	Glu	Ala	Glu	Lys	Gln	Leu	Ser	Leu	Glu	Leu	Glu	Lys	Asn	305	310	315	320
Glu	Gln	Arg	Gln	Ile	Ala	Ser	Val	Ile	Arg	Ala	Pro	Val	Ser	Gly	Thr	325	330	335	
Val	Gln	Gln	Leu	Lys	Thr	His	Thr	Val	Gly	Gly	Val	Val	Thr	Thr	Ala	340	345	350	
Glu	Thr	Leu	Met	Val	Ile	Ala	Pro	Glu	Asp	Asp	Val	Leu	Glu	Val	Thr	355	360	365	

Ala Leu Ile Gln Asn Lys Asp Ile Gly Phe Ile Glu Val Gly Gln Asp
370 375 380

Ala Val Ile Lys Val Glu Thr Phe Pro Tyr Thr Arg Tyr Gly Tyr Leu
385 390 395 400

Met Gly Lys Val Lys Asn Ile Thr Leu Glu Ala Ile Glu His Pro Gln
405 410 415

Leu Gly Leu Val Phe Asn Ser Ile Ile Ser Ile Asp Arg Lys Thr Leu
420 425 430

Ser Gly Lys Asp Gly Lys Glu Ile Glu Leu Gly Ser Gly Met Ser Val
435 440 445

Thr Ala Glu Ile Lys Thr Gly Glu Arg Ser Val Ile Ser Tyr Leu Leu
450 455 460

Ser Pro Leu Glu Glu Ser Val Ser Glu Ser Leu Arg Glu Arg
465 470 475

<210> 40

<211> 478

<212> PRT

<213> Escherichia coli

<400> 40

Met Lys Thr Trp Leu Met Gly Phe Ser Glu Phe Leu Leu Arg Tyr Lys
1 5 10 15

Leu Val Trp Ser Glu Thr Trp Lys Ile Arg Lys Gln Leu Asp Thr Pro
20 25 30

Val Arg Glu Lys Asp Glu Asn Glu Phe Leu Pro Ala His Leu Glu Leu
35 40 45

Ile Glu Thr Pro Val Ser Arg Arg Pro Arg Leu Val Ala Tyr Phe Ile
50 55 60

Met Gly Phe Leu Val Ile Ala Phe Ile Leu Ser Val Leu Gly Gln Val
65 70 75 80

Glu Ile Val Ala Thr Ala Asn Gly Lys Leu Thr Leu Ser Gly Arg Ser
85 90 95

Lys Glu Ile Lys Pro Ile Glu Asn Ser Ile Val Lys Glu Ile Ile Val
100 105 110

Lys Glu Gly Glu Ser Val Arg Lys Gly Asp Val Leu Leu Lys Leu Thr
115 120 125

Ala Leu Gly Ala Glu Ala Asp Thr Leu Lys Thr Gln Ser Ser Leu Leu
130 135 140

Gln Ala Arg Leu Glu Gln Ile Arg Tyr Gln Ile Leu Ser Arg Ser Ile
145 150 155 160

Glu	Leu	Asn	Lys	Leu	Pro	Glu	Leu	Lys	Leu	Pro	Asp	Glu	Pro	Tyr	Phe	165	170	175
Gln	Asn	Val	Ser	Glu	Glu	Glu	Val	Leu	Arg	Leu	Thr	Ser	Leu	Ile	Lys	180	185	190
Glu	Gln	Phe	Ser	Thr	Trp	Gln	Asn	Gln	Lys	Tyr	Gln	Lys	Glu	Leu	Asn	195	200	205
Leu	Asp	Lys	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ile	Leu	Ala	Arg	Ile	Asn	210	215	220
Arg	Tyr	Glu	Asn	Val	Ser	Arg	Val	Glu	Lys	Ser	Arg	Leu	Asp	Asp	Phe	225	230	235
Arg	Ser	Leu	Leu	His	Lys	Gln	Ala	Ile	Ala	Lys	His	Ala	Val	Leu	Glu	245	250	255
Gln	Glu	Asn	Lys	Tyr	Val	Glu	Ala	Ala	Asn	Glu	Leu	Arg	Val	Tyr	Lys	260	265	270
Ser	Gln	Leu	Glu	Gln	Ile	Glu	Ser	Glu	Ile	Leu	Ser	Ala	Lys	Glu	Glu	275	280	285
Tyr	Gln	Leu	Val	Thr	Gln	Leu	Phe	Lys	Asn	Glu	Ile	Leu	Asp	Lys	Leu	290	295	300
Arg	Gln	Thr	Thr	Asp	Ser	Ile	Glu	Leu	Leu	Thr	Leu	Glu	Leu	Glu	Lys	305	310	315
Asn	Glu	Glu	Arg	Gln	Gln	Ala	Ser	Val	Ile	Arg	Ala	Pro	Val	Ser	Gly	325	330	335
Lys	Val	Gln	Gln	Leu	Lys	Val	His	Thr	Glu	Gly	Gly	Val	Val	Thr	Thr	340	345	350
Ala	Glu	Thr	Leu	Met	Val	Ile	Val	Pro	Glu	Asp	Asp	Thr	Leu	Glu	Val	355	360	365
Thr	Ala	Leu	Val	Gln	Asn	Lys	Asp	Ile	Gly	Phe	Ile	Asn	Val	Gly	Gln	370	375	380
Asn	Ala	Ile	Ile	Lys	Val	Glu	Ala	Phe	Pro	Tyr	Thr	Arg	Tyr	Gly	Tyr	385	390	395
Leu	Val	Gly	Lys	Val	Lys	Asn	Ile	Asn	Leu	Asp	Ala	Ile	Glu	Asp	Gln	405	410	415
Lys	Leu	Gly	Leu	Val	Phe	Asn	Val	Ile	Val	Ser	Val	Glu	Glu	Asn	Asp	420	425	430
Leu	Ser	Thr	Gly	Asn	Lys	His	Ile	Pro	Leu	Ser	Ser	Gly	Met	Ala	Val	435	440	445
Thr	Ala	Glu	Ile	Lys	Thr	Gly	Met	Arg	Ser	Val	Ile	Ser	Tyr	Leu	Leu	450	455	460

Ser Pro Leu Glu Glu Ser Val Thr Glu Ser Leu His Glu Arg
465 470 475

<210> 41

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<220>

<221> modified_base

<222> (14)

<223> a, t, c, g, other or unknown

<400> 41

tagtaaatta aatnactwaa cact